

06-MAY-1999; 99US-0306111.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D;
Treacy M, DiBlasio-Smith E, Widom A;

WPI: 2000-205978/18.
N-PSDB; 293173.

New polynucleotides encoding secreted human proteins, useful for treating e.g. broken bones, craniofacial defects, periodontal disease, osteoporosis, burns, incisions or ulcers -

Claim 32: Page 99-100; 105pp; English

The human chordin related protein and polynucleotides encoding them are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions which involve defects in cartilage, bone or connective tissue formation and damage to cartilage, bone or connective tissue, e.g. broken bones, congenital, trauma-induced, or oncologic-resection-induced craniofacial defects, periodontal disease, defects in the periodontal ligament or attachment apparatus, damage to the periodontal ligament or attachment apparatus, osteoporosis, burns, incisions or ulcers. The proteins may also affect neurons, astrocytic, and glial cell survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival and repair. The proteins may also be useful for the treatment of conditions related to other types of tissue, such as nerve, epidermis, muscle, and other organs such as liver, brain, lung, cardiac, pancreas, and kidney tissue. The proteins may further be useful for the treatment of relatively undifferentiated cell populations, such as embryonic cells, or stem cells, to enhance growth and/or differentiation of the cells. The proteins may also have other useful properties characteristic of the IGF-beta superfamily of proteins. Such properties include angiogenic, chemotactic, and/or chemoattractant properties, and effects on cells including induction or inhibition of collagen synthesis, fibrosis, differentiation responses, cell proliferative responses, and responses involving cell adhesion, migration, and extracellular matrices. These properties make the proteins potential agents for wound healing, reduction of fibrosis, and reduction of scar tissue formation. Chordin-related proteins may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs. Chordin-related proteins may also be useful in modulating hematopoiesis by inducing the differentiation of erythroid cells, for suppressing the development of gonadal tumors, or for augmenting the activity of BMPs. The proteins may also have value as a dietary supplement, or as a component of cell culture media.

Sequence 457 AA;

Query Match 6.2%; Score 92.5; DB 21; Length 457;
Best Local Similarity 25.0%; Pred. No. 0.25;
Matches 38; Conservative 22; Mismatches 57; Indels 35; Gaps 7;

127 YDVALDLILQVDASNSE-----MFTDEQHEMVESAAMEL--YGLIH-VRYILITKG 174

12 Yifslilillegskteqvhse:ymfkdqkkyvqerwhylepyalvcvncicseag 71

175 MAAMTERYKNCDFGRFCGSCQLPVGQSDIPRSSTVKIYCPKCEDISYPSKFGN 234

72 nvl-----csrrvcnvhc:spvhip-----hlcpcpcpdsfpvnmkvt 112

235 IDGAYFGTTTPH--LFLM--TYGNLKFQKFTQ 262

113 kseeYngtYqhqlfvaegltgn:qpnqctq 144

RESULI 4

Y53035

ID Y53035 standard; Protein; 457 AA.

AC Y53035;

DT 29-FEB-2000 (first entry)

XX Human secreted protein clone dw665_4 protein sequence SEQ ID NO:76.

XX Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; suppression;
KW haematopoiesis regulation; tissue growth; activin; inhibin;
KW chemotactic; chemokinetic; haemostatic; thrombolytic; receptor;
KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

XX Homo sapiens.

XX W09957132-AL.

XX 11-NOV-1999.

XX 07-MAY-1999; 99WO-US09970.

XX 07-MAY-1998; 98US-0084564.

XX 02-JUN-1998; 98US-0087645.

XX 22-JUL-1998; 98US-0093712.

XX 31-JUL-1998; 98US-0094935.

XX 10-AUG-1998; 98US-0095880.

XX 11-AUG-1998; 98US-0096068.

XX 06-MAY-1999; 99US-0096068.

XX (GENY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;

PI DiBlasio-Smith E, Widom A;

XX WPI: 2000-052937/04.

DR N-PSDB; 233353.

XX New polynucleotides encoding secreted human proteins, derived from

PT adult placenta, adult retina, fetal brain, fetal

XX Claim 85; Page 430-432; 492pp; English.

XX The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. 233316 to 233373 encode human secreted proteins, and Y52998 to Y53060 represent human secreted proteins, given in the present invention.

XX Sequence 457 AA;

Query Match 6.2%; Score 92.5; DB 21; Length 457;

Best Local Similarity 25.0%; Pred. No. 0.25;

Matches 38; Conservative 22; Mismatches 57; Indels 35; Gaps 7;

QY 127 YDVALDLILQVDASNSE-----MFTDEQHEMVESAAMEL--YGLIH-VRYILITKG 174

12 yifsliflllggkteqvkhssetymfkdqkyrgerwpylepvglyvncieseng 71
175 MAAMTEKYKNCDFGRPRVFCGGCLPVGSCIDPRSTVKYCPKCECISYPRSKFOGN 234
772 nvl-----csrvcpnvhscspnhp-----hlcepcpdsppvinkvts 112
235 IFCAYGTTTFRPH-LFLM--TYGNIKKPKQPTQ 262
113 kseevngtttyqgelfvaeaglfqnrqpnqctq 144

ULT 5
668
Y28668 standard; Protein; 316 AA.

Y28668;

26-OCT-1999 (first entry)

Salmonella enteritidis wild type orfa encoded protein.

Wild type orfa; Salmonella chromosome; Salmonella specific loop; orfx;
orfv; orfw; f76; 0468; Salmonella pathogenicity islet; sifa gene;
Salmonella typhimurium; immune response; genetically modified; vaccine;
Salmonella induced filament; attenuated; humoral; local; cellular;
tumour; hormone; allergen; toxin; pathogen.

Salmonella enteritidis.

W09937759-A2.

29-JUL-1999.

22-JAN-1999; 99WO-BE00007.

24-Sep-1998; 98SP-0870202.

22-JAN-1998; 98SP-0870019.

(UYVR-) UNIV VRLJE BRUSSEL.

De Greve H, Gubbels E, Hernalsteens J;

WPI; 1999-479047/40.

N-PSDB; X89748.

Vaccine containing attenuated Salmonella strain, for generating
protective immune response to Salmonella or other antigens

Example 2; Page 60-61; 78pp; English.

The present protein sequence is encoded by the orfa wild type DNA which
lies within a region of the Salmonella chromosome. The orfa is located
at one end of the 3417bp Salmonella specific loop comprising Salmonella
pathogenicity islet and including orfx, orfa, orfv and orfw. The loop is
flanked by sequences that show homology with the E.coli open reading
frames f76 and 0468. The orfa encoded protein was found to have 26.7%
homology with the S.typhimurium sifa gene product involved in the
production of "Salmonella induced filaments" in infected epithelial cells
and is required for the virulence of this bacterium. A live, genetically
modified Salmonella strain comprising a modification in this wild type
sequence becomes avirulent and can be used to identify virulent
Salmonella strains. Modified attenuated strains can be used to prepare
vaccines for inducing an immune response (humoral, local and cellular)
against infections induced by Salmonella strains and/or other pathogens,
tumours, hormones, allergens, toxins, etc.

Sequence 316 AA;

Query Match 5.9%; Score 88; DB 20; Length 316;
Best Local Similarity 23.0%; Prod. No. 0.44;
Matches 57; Conservative 30; Mismatches 101; Indels 60; Gaps 10;

QY 35 KLEKSTSTSTTSRVFSS-----KKKDPFSFTSTKT-----QLPDVESEINSEGSUVSGSE 84
DB 11 ksmf'ssaisqrsflllwerikdfcdqrstadykkelcdvasppdaq----- 62
QY 85 GDOTSWISWFCNL-----RGNDFP-----CEVEDYIOB---DFNLGG:SGQVPYY 127
DB 63 ----Lfdlfcalyelsspscrgnfhrfhykdaecytnfkdgodipicivirghyy 118
QY 128 DYALD---LILDVDASNSEMTDEQHMEVESAAEMLYGLIHRVYLLITKG----- 174
DB 119 ydlmrtvlcvdtqpahlkrysditkastyveeclclfcprllslsggltfpxdlkm 178
QY 175 ----MAAMTEKYKNCDFGRPRVFCGGCLPVGSCIDPRSTV---KIYCPKCECISY 226
DB 179 iketliamaekgnldwkqerkaaisrrinlgiaqadvppiddaiknkaakvientnl 238
QY 227 PRSKFOGN 234
DB 239 knaafepn 246

RESULT 6

Y06221

ID Y06221 standard; Protein; 559 AA.

XX AC Y06221;

DI 15-AUG-1999 (first entry)

XX FHRC E. coli; translocated intimin receptor (Tir).

XX DE Tir; translocated intimin receptor; Hp90; enterohaemorrhagic;

XX KW EHEC; infection; diagnosis; vaccine.

XX OS Escherichia coli.

XX Key Location/Qualifiers

FI Misc-difference 453

FT /note- "encoded by codon of 1 apparent nucleotide,
causing frameshift in the DNA sequence"

XX W09924576-A1.

XX 20-MAY-1999.

XX PF 10-NOV-1998; 98WO-CA01042.

XX PR 12-NOV-1997; 97US-0065130.

XX (UYVR-) UNIV BRITISH COLUMBIA.

XX Devlinney R, Finlay BB, Kenny B, Stein M;

XX WP1; 1999-337712/28.

DB N-PSDB; X58859.

PI New translocated intimin receptor useful for treating infection by
enteropathogenic or enterohaemorrhagic Escherichia coli

PS Claim 7; Page 55-58; 91pp; English.

XX The present sequence represents Tir, a novel translocated intimin
receptor (formerly termed Hp90) from an enterohaemorrhagic
Escherichia coli (EHEC) strain. The sequence was deduced from an
isolated tir polynucleotide (see X58859). Tir proteins are
secreted by attaching and effacing pathogens such as EHEC and EPEC
(see Y06220) E. coli. The bacterial pathogens insert their own
receptors into mammalian cell surfaces, to which the pathogen then
adheres to trigger additional host signaling events and actin
nucleation. Diagnosis of disease caused by pathogenic E. coli can
be performed by use of antibodies that bind to Tir to detect the
protein or the use of nucleic acid probes for detection of nucleic

acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing *E. coli* are provided. A method of immunising a host with Tir to induce a protective immune response is also provided. In addition, Tir fusion proteins can be used in attenuated *E. coli* to induce a cell-mediated immune response to other polypeptides, e.g. antigens. A method for screening for compounds which interfere with the binding of bacterial pathogens to their receptors is further provided.

Sequence 559 AA:

Query Match 5.9%; Score 57; DB 20; Length 559;
Best Local Similarity 30.4%; Pred. No. 1.3;
Matches 31; Conservative 19; Mismatches 42; Indels 10; Gaps 4;
6 SGGGGGSRSEILGGAIDRKRINDALNKK--LEKSSSTTSRVFSKDKDPFSFIST 62
358 ssgagvglsгалilggig-vavtaalhrkkgvgqgttttttttsartvenkpannt 416
63 KTG-----LHVSEISDSGSDVSGSGB--DTSWISWPCNER 96
417 padgnvdtppsedtmesrismastestfdtsiaqqparir 459

RESULT 7

W87760 standard; Protein: 784 AA.
W87760:

29-MAR-1999 (first entry)

Soybean lysine ketoglutarate reductase.

Lysine ketoglutarate reductase; saccharopine dehydrogenase;
transgenic plant; seed; soybean.

Glycine max.

W09842831-A2.

01-OCT-1998.

27-MAR-1998; 98WO-US06051.

27-MAR-1997; 97US-0824627.

(DUPO) DU PONT DE NEMOURS & CO E I.

Epelbaum SU, Falco SC, McDevitt RB;

WPI: 1999-045149/04.

N-PSDB: V99562.

Nucleic acids and chimeric genes for increasing seed lysine content - comprise sequence encoding all or part of lysine ketoglutarate reductase, useful to improve nutritional quality of seeds from transformed plants

Claim 2; Page 186-188; 231pp; English.

This is the amino acid sequence of a soybean near full-length lysine ketoglutarate reductase (LKR) or saccharopine dehydrogenase (SDH). It was deduced from cDNA (see V99562) obtained from developing seed mRNA by PCR and RACE. Isolated nucleic acids comprising sequences encoding all or part of plant LKR enzymes are new. Also claimed are: (1) a chimeric gene comprising the fragment (or a subfragment) operably linked to a seed specific regulator, where the chimeric gene reduces LKR activity in plant seeds transformed with it; (2) plant cells and seeds in which LKR

CC activity is reduced due to a mutation in the gene encoding LKR or
CC transformator with the chimeric gene; (3) a nucleic acid fragment
CC comprising: (i) chimeric gene above, and (ii) a second chimeric gene,
CC in which a nucleic acid fragment encoding dihydrodipicolinic acid
CC synthase (DHPS) substantially insensitive to lysine inhibition is
CC operably linked to a plant chloroplast transit sequence and to a
CC plant seed-specific regulatory sequence; (4) plants comprising in
CC genome (i) and (ii), especially as fragment of (2); and (5) seeds
CC from (3). The chimeric genes can be used to produce plant cells
CC and seeds with reduced LKR activity, especially in Arabidopsis,
CC corn, soybean, rapeseed, wheat and rice (claimed). LKR is
CC important in controlling free lysine accumulation in plant seeds.
CC LKR activity reduction may be achieved by cloning the claimed
CC fragment, preparing a chimeric gene for cosuppression of LKR,
CC expression of antisense RNA for LKR, and transforming plants with
CC the chimeric gene.

XX Sequence 784 AA:

Query Match 5.8%; Score 85.5; DB 20; Length 784;
Best Local Similarity 20.1%; Pred. No. 2.9;
Matches 57; Conservative 42; Mismatches 103; Indels 81; Gaps 14;
QY 14 SRSEILGGAIDRKRINDALNKKLEKSSSTTSRVFSKDKDPFSFTSTKTOLPDVESET 73
DB 243 sfseevga-dtravldqldstataisptehdr-fsnqssksiklgkveenglekcs 300
QY 74 D-----SEGSNVSGSGGDDISWISWFCNLKGNDFCEVDEYI----- 111
DB 301 dprkkaavllagrvccpaemlssfgprss-sqwykclldrecqtdveivgslyl 359
QY 112 -----QDEFNICGILSGQVPYYDYALDITLDVDCASNSMPTDEQHE 151
DB 360 kdaeqtveqipnvtgqlqdvmdranlckvisq-----dvvi-----slppsch 405
QY 152 MVESAA-EMLYGLIHVRYILTTKGMAAMTEKYKNC-----DFGRCPRVFCCG--QSCLP 202
DB 406 lvanacieikkhltvtsyv--dssmslnldkakdagitilgemglpgi---ghumamkm 460
QY 203 VQSDIPRSSTVLYCPKCEDISYPRS-----KFGQNIIDGA 238
DB 461 inqahv-rkgkksfscgglpspeaanplaykfswnpqa 502

RESULT 8

W81168 standard; Protein: 947 AA.
ID W81168

XX AC W81168;

XX DT 05-MAR-1999 (first entry)

XX DE Transcriptional regulatory factor RING3.

XX KW Human; transcriptional regulatory factor; RING3; TSB; cancer;
XX testis specific bromodomain; testicular cell proliferation.

XX OS Homo sapiens.

XX XN W09848015-A1.

XX XX 29-OCT-1998.

XX XX 17-APR-1998; 98WO-JP01782.

XX PR 18-APR-1997; 97JP-0116402.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Jones MH;

XX XX WPI: 1998-583658/49.

DR

Tureci O;

•

DBL gene; Duffy-binding like gene; cbl-1; Duffy Antigen Binding Protein; DABP; Sialic Acid Binding Protein; SAMP; malaria; vaccine; immunisation; protozoacide.

This is a truncated BLM protein encoded by a mutant gene sequence isolated from a German Bloom's Syndrome sufferer designated "112(NaSch)". The substitution of the base A at the position 889 of the wild type H1-5' gene to the base T results in a stop codon at amino acid position 272. This was one of the seven unique mutations which were identified in a study of 10 people with Bloom's Syndrome. Based on the various mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene. Note: The present sequence does not appear in the specification; it has been made by modifying the H1-5' wild type BLM sequence which is provided in Figure 2 (W15264).

Sequence 271 AA:

Query Match 5.6%; Score 83; DB 18; Length 271;
Best Local Similarity 21.7%; Pred. No. 1.2;
Matches 36; Conservative 17; Mismatches 41; Indels 72; Gaps 5;
26 KRINDALNKKLEKSTSTTSRVPSKSKKDPSTSTST----- 62
129 kksrdtaikklefsspsdlsistindwdmdtdtsetsksfvtppqshfvrystaqskk 188
63 -----KTGLPVESEKIDSEGSNWSGSDDTFSWISWFCNLKGNDFPC-- 104
189 gkrnlfkaqlttrvkvktrpfpse--seqid:eedkddsewis-----sdvaid 239
105 -----EVEDDYIQDQFNICGLSGQVYYDYALDILLDVDASNSE 143
240 dypiaevhinedaqcsd-----skthlederduse 270

rich completed: November 15, 2000, 13:23:47
time: 2938 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

protein - protein search, using sw model

on: November 15, 2000, 12:57:15 ; Search time 36.78 seconds
(without alignments)
485.450 Million cell updates/sec

ie: US-09-359-C26-2
foot score: 1486
quence: 1 MYKRSGGGGSGSRSEILG.....PQKPIQSVVPKIFGKVKHP 276

oring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

ched: 182106 seqs, 63460219 residues

al number of hits satisfying chosen parameters: 182106

imum DB seq length: 0
imum DB seq length: 200000000
st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 65:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1486	100.0	276	2	T49220	regulatory subunit
2	1294	87.1	283	2	T01595	casein kinase II
3	1039.5	70.0	287	2	S47967	casein kinase II
4	1018	68.5	282	2	S47968	casein kinase II
5	621	41.8	215	2	A39459	casein kinase II
6	621	41.8	215	2	C38611	casein kinase II
7	621	41.8	215	2	JNC556	casein kinase II
8	621	41.8	215	2	S14724	casein kinase II
9	621	41.8	215	2	S23405	casein kinase II
10	621	41.8	215	3	JC7269	protein kinase (EC
11	615	41.4	209	2	A25828	casein kinase II
12	604	40.6	231	2	S50126	casein kinase II
13	599	40.3	235	2	T24317	hypothetical prote
14	597.5	40.2	234	2	T24320	hypothetical prote
15	588.5	39.6	234	2	A41036	casein kinase II
16	543	35.5	156	2	S14725	casein kinase II
17	514.5	34.6	258	2	A54307	casein kinase II
18	477.5	32.1	254	2	T40159	casein kinase II
19	446	30.9	278	2	A56421	casein kinase II
20	370.5	24.9	172	2	S24397	stellate protein
21	369.5	24.9	172	2	S24398	stellate protein
22	95.5	6.4	1274	2	T02636	PI protein homolog
23	93.5	6.3	937	2	S58335	hypally regulated
24	92.5	6.2	515	2	T40809	glutamyl-tRNA redu
25	89	6.0	436	2	T45602	glucosyltransferas
26	89	6.0	1211	2	T08540	hypothetical prote
27	87	5.9	852	2	S48945	hypothetical prote
28	86.5	5.8	408	2	T25524	hypothetical prote
29	86.5	5.8	438	2	T15789	probable secreted

DNA-binding protei
DNA-binding protei
DNA polymerase III
hypothetical prote
ubiquitin-specific
rod cyclic nucleot
surface array prot
SRP40 protein - ye
Bloom's syndrome r
lactocepin (EC 3.4
hypothetical prote
Duffy receptor - p
hypothetical prote
periplasmic cell d
probable membrane

ALIGNMENTS

RESULT 1

T49220
regulatory subunit of protein kinase CK2 - Arabidopsis thaliana
N:Alternate names: protein F27H5.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 *sequence_revision 02-Jun-2000 *text_change 02-Jun-2000
C:Accession: T49220
R:Rieser, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49220
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <RIE>
A:Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.40
A:Experimental source: cultivar Columbia; BAC clone F27H5
C:Genetics:
A:Gene: ATSP:F27H5.40
A:Map position: 3
A:Introns: 69/1; 142/1; 178/3; 234/1

Query Match 100.0%; Score 1486; DB 2; Length 276;

Best Local Similarity 100.0%; Pred No. 5.8e-118; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKRSGGGGSGSRSEILGGAIDRKKINDALNKKLEKSTSTSTTSRVFSSKDKDPFSFT 60

DB 1 MYKRSGGGGSGSGSRSEILGGAIDRKKINDALNKKLEKSTSTSTTSRVFSSKDKDPFSFT 60

QY 61 STKTQLPDVSEFTDSGSGSVSGSGDDTSWISFNCNLGNDFCEVDEYIQDDFNLCGL 120

DB 61 STKTQLPDVSEFTDSGSGSVSGSGDDTSWISFNCNLGNDFCEVDEYIQDDFNLCGL 120

QY 121 SGQVPYDYALDJLJLWVDASNSEMTDEQHEMVESAEMLYGLIHVRYITITKGMAAMTE 180

DB 121 SGQVPYDYALDJLJLWVDASNSEMTDEQHEMVESAEMLYGLIHVRYITITKGMAAMTE 180

QY 181 KYKNCDFGRCPRVCCGQSCIPVCGSDTPHSSIVKLYCPKCEDISYPRSKFQGNIDGAVF 240

DB 181 KYKNCDFGRCPRVCCGQSCIPVCGSDTPHSSIVKLYCPKCEDISYPRSKFQGNIDGAVF 240

QY 241 GTTFPHLFTMTYGNLKPQKPTQSYVPKIFGKVKHP 276

DB 241 GTTFPHLFTMTYGNLKPQKPTQSYVPKIFGKVKHP 276

RESULT 2

T01595
casein kinase II (EC 2.7.1.-) beta chain F16B22.17 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 *sequence_revision 19-Feb-1999 *text_change 11-Jan-2000

QY	61	STKTQL-----	-----PDVSEITDSEGDVSGSKGDDTWNLSWFC	96
DB	47	TITANLIGKQSQNNINHRORSASLKNNTVSDDESITDSESDVSGSGDGTISWLSWFC	106	
QY	96	NLRKGNDFCEVDDEYTDQDFNLCLGSLGQVPPYDYALDLILDVDASNSEMTDQEHQEMVES	155	
DB	107	NLRKGNDFCEVDDDYLDQDFNLCLGSLSLPYPPYFAYALDILDVSSOGEMFTBEGNELIES	166	
QY	156	AAEMLYGLLHVRYILTTKGMAAMTEYKKNCDRGCRPFVCCGQSCULPVGQSDIPRSSTVK	215	
DB	167	AAEMLYGLLHARYILTSKLAAMDLYKKNDFGRCPRVCCGQPCULPVGQSQLPRSSSTVK	226	
QY	216	IYCPKCEDISYPRSKFGNIDGAYFGTITPLFLMTYGNLKPCKPQTQSYVPKLFGRKVKHK	275	
DB	227	IYCPKCEDIYPRSKYQGNIDGAYFGTTTFLFLMTYGHCLKPAKATQNYQVRVEGRFLHK	286	
QY	276	P 276		
DB	287	P 287		

RESULI 4
 S47968
 cscin kinase II (EC 2.7.1.-) beta chalt: CKB2 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Variety: Columbia
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
 C:Accession: S47968; C71446
 R:Collinge, M.A.; Walker, J.C.
 Plant Mol. Biol. 25, 649-658, 1994
 A:Title: Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 A:Reference number: S47967; M01D:9439478
 A:Accession: S47968
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-282 <COL>
 A:Cross-references: HMBL:U03984; NID:g467974; P:D:g467975
 P:Bevan, M.; Hancock, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Berg
 T.; Wedler, H.; Wedler, E.; Wambutt, R.; Weizenssger, T.; Pohl, T.M.; Te
 avannag, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer,
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.;
 chraft, A.; Mccriss, I.; Jones, J.D.G.; Eneva, T.; Palme, K.; Bonas, V.; Re
 C.; Chlwaatzis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of A
 A:Reference number: A7400; M01D:98121113

C:Gene: CRB2
C:Genetics:
A:Gere: CRB2
C:Map position: 4C09-403845
C:Superfamily: human casein kinase II beta chain
C:Keywords: phosphotransferase; protein kinase

Query Match	68.5%	Score 1018	DB 2:	Length 282:
Best Local Similarity	65.5%	pred. No. 1.7e-78:		
Matches 190:	Conservative 41:	Mismatches 37:	Indels 22:	Caps

[illegible]

QY 143 EMFTDEQHEKVESAAEMLYGLIHVRYILITTKGMAAMTEKYKNCDFGRCPRVFCGGSCLP 202
 DB 62 LEENPNQSDLIETQAAEMLYGLIHARYILITNKGIAQMLEKYQQGDFGYGCPRVYCNQPMPLP 121
 QY 203 VQOSDIPRSSTVKIYCPKCEDISYPRSKFQGNIDGAYFGTTFPHLFLMTYGNLKPQKPTQ 262
 DB 122 IGLSDIPGEMAVKLYCPKCMNDVYTPKSSRRHHHTDGAFTGTFPHLMFLMVHPEYRPRKPAN 181
 QY 263 SYVPKIFGFKVH 274
 DB 182 QFVPRLYGFKIH 193
 RESULT 6
 C38611
 C:Species: Gallus gallus (chicken)
 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 10-Dec-1999
 C:Accession: C38611
 R:Maridor, G.; Park, W.; Krek, W.; Nigg, E.A.
 J. Biol. Chem. 266, 2362-2368, 1991
 A:Title: Casein kinase II. cDNA sequences, developmental expression, and tissue distribution
 A:Reference number: A38611; MUID:G1115855
 A:Accession: C38611
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-215 <NAR>
 A:Cross-references: GH:M59458; GB:J05738; NID:G211535; PID:G211536
 C:Superfamily: human casein kinase II beta chain
 C:Keywords: autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

Query Match 41.8%; Score 621; DB 2; Length 215;
 Best Local Similarity 55.7%; Pred. No. 3,60-45;
 Matches 107; Conservative 31; Mismatches 54; Indels 0; Gaps 0;

QY 83 SEGQDTSWISWFCNLRGNDFCFEVDYIQQDNLCGLSGQVPYDYVALCLILDVDASNS 142
 DB 2 SSSEFWSISWFCNLRGNDFCFEVDYIQQDNLCGLSGQVPYDYVALCLILDVDASNS 142
 QY 143 EMFTDEQHEKVESAAEMLYGLIHVRYILITTKGMAAMTEKYKNCDFGRCPRVFCGGSCLP 202
 DB 62 LEENPNQSDLIETQAAEMLYGLIHARYILITNKGIAQMLEKYQQGDFGYGCPRVYCNQPMPLP 121
 QY 203 VQOSDIPRSSTVKIYCPKCEDISYPRSKFQGNIDGAYFGTTFPHLFLMTYGNLKPQKPTQ 262
 DB 122 IGLSDIPGEMAVKLYCPKCMNDVYTPKSSRRHHHTDGAFTGTFPHLMFLMVHPEYRPRKPAN 181
 QY 263 SYVPKIFGFKVH 274
 DB 182 QFVPRLYGFKIH 193
 RESULT 7
 JN0556
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Dec-1999
 C:Accession: JN0556
 R:Gupta, S.K.; Singh, G.P.
 Gene 124, 287-290, 1993
 A:Title: PCR cloning and sequence of two cDNAs encoding the alpha and beta subunits of casein kinase II (EC 2.7.1.1) beta chain - rabbit
 A:Reference number: JN0555; MUID:G3185937
 A:Accession: JN0556
 A:Molecule type: mRNA
 A:Residues: 1-215 <GUP>
 A:Cross-references: GH:S56242; NID:G298366; PIDN:AAB25555.1; PID:G298367
 C:Superfamily: human casein kinase II beta chain
 C:Keywords: autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
 F:2/Binding site: phosphate (Ser) (covalent) #status predicted

122 PMLPVGLSDIAHTRKSVKLYCPRCEDVYTPKSQLRHASIDCAYFGTSPHMLFQVYPELAVP 181

arch completed: November 15, 2000, 13:25:10
b time: 1675 sec

seqCore version 4.5
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protein - protein search, using sw model

on: November 15, 2000, 13:23:50 : Search time 29.75 Seconds
(without alignments)
306,700 Million cell updates/sec

ie: US-09-359-026-2

fect score: 1486

quence: 1 MYKERSGGGGSSRSSEILG.....PQKPTQSVVPK:FG:VKHP 276

oring table: BLCSUM62

Gapo 10.0 , Gapo 0.5

arched: 87953 seqs, 31947951 residues

ta: number of hits satisfying chosen parameters: 87953

imum DB seq length: 0

imum DB seq length: 200000000

st-processing: Minimum Match 0%

Listing first 45 summaries

atabase : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1485	100.0	276	1 KC2D_ARATH	061275 arabidopsis
2	1294	87.1	283	1 KC2E_ARATH	060507 arabidopsis
3	1039.5	70.0	287	1 KC2B_ARATH	040228 arabidopsis
4	1018	68.5	282	1 KC2C_ARATH	040229 arabidopsis
5	621	41.8	215	1 KC2B_BRARE	091388 bractydanic
6	621	41.8	215	1 KC2B_HUMAN	138522 homo sapien
7	621	41.8	215	1 KC2B_XENLA	28021 xenopus lac
8	612	41.2	215	1 KC2B_DROME	08182 drosophila
9	604	40.6	231	1 KC2B_SCHPO	040232 schizosacch
10	592	39.8	221	1 KC2B_SPOFR	076485 spodoptera
11	588.5	39.6	234	1 KC2L_CABEL	028548 caenorhabdi
12	538	36.2	219	1 KC2C_DROME	096853 drosophila
13	514.5	34.6	238	1 KC2C_YEAST	138930 saccharomyc
14	445	30.0	278	1 KC2B_YEAST	043639 saccharomyc
15	445	29.9	294	1 KC2B_CANAL	059906 candida alb
16	434.5	29.2	219	1 SSL_DROME	024536 drosophila
17	370.5	24.9	172	1 STBL_DROME	015021 drosophila
18	92.5	6.2	315	1 HEM_GLOIO	059282 clostridium
19	92.5	6.2	937	1 HYR1_CANAL	046591 candida alb
20	87	5.9	852	1 YBQ3_YEAST	0386.4 saccharomyc
21	84	5.7	1272	1 YBP2_YEAST	001476 saccharomyc
22	83.5	5.6	691	1 CNGL_CANFA	028279 canis famil
23	83	5.6	406	1 SHM_YEAST	032583 saccharomyc
24	83	5.6	1417	1 BUM_HUMAN	034132 homo sapien
25	83	5.6	1902	1 P2P_LACPA	002470 lactobacilli
26	82.5	5.6	1070	1 PVDR_PLAVS	022290 plasmodium
27	82	5.5	532	1 YHB7_YEAST	038745 saccharomyc
28	81	5.5	2411	1 DAB_DROME	098081 drosophila
29	80.5	5.4	346	1 IMPX_YEAST	032351 saccharomyc
30	80	5.4	555	1 NASV_PTCAN	021360 picnia angu
31	80	5.4	770	1 KiPA_FEMFI	028739 omericella
32	80	5.4	1902	1 FLP_LACLC	016271 lactococcus
33	79.5	5.3	320	1 VP10_RGDV	029078 rice gall d

34	79.5	5.3	827	1 CSG_HALVO	P25062 halobacteri
35	79.5	5.3	933	1 SLAP_CAMFE	P35827 campylobact
36	78.5	5.3	490	1 TWST_DROME	P10627 drosophila
37	78.5	5.3	558	1 YCX9_ASTLO	P34782 astasia ion
38	78.5	5.3	1002	1 YEMA_DROME	P25992 drosophila
39	78	5.2	510	1 DMP1_BOVIN	Q95120 bos taurus
40	78	5.2	656	1 GPH1_CANAL	P43079 candida alb
41	78	5.2	1902	1 P2P_LACLA	P15293 lactococcus
42	78	5.2	1902	1 P3P_LACLC	P15292 lactococcus
43	77.5	5.2	469	1 DP02_HUMAN	P49005 homo sapien
44	77.5	5.2	564	1 HEMA_TABUD	P19694 influenza a
45	77.5	5.2	690	1 CNGL_BOVIN	Q00194 bos taurus

ALIGNMENTS

RESULT					
KC2D_ARATH					
ID	KC2D_ARATH	STANDARD;	PRI:	276 AA.	
AC	G81275;				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	CASEIN KINASE II BETA-5 CHAIN (CK II) (EC 2.7.1.37).				
GN	CKB3				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;				
OC	Brassicales; Brassicaceae; Arabidopsis.				
RN	[1]				
RF	SEQUENCE FROM N.A.				
RX	MEDLINE: 98393763.				
RA	Sugano S., Andronis C., Green R.M., Wang Z.Y., Tobin E.M.;				
RI	"Protein kinase CK2 interacts with and phosphorylates the Arabidopsis				
RI	circadian clock-associated 1 protein.";				
RI	Proc. Natl. Acad. Sci. U.S.A. 95:11020-11025(1998).				
CC	-!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC				
CC	ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).				
CC	-!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND				
CC	TWO BETA-TYPE CHAINS.				
CC	-!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: AF068318; AAC33896.1; .				
CC	INTERPRO: IPR000704; .				
DR	PFAM: PF01214; CK.II.beta.1.				
DR	PRINTS: PR00472; CASNKNASE11.				
DR	PROSITE: PS0131; CK2_HETA; 1.				
KW	Transferase; Serine/threonine-protein kinase; Phosphorylation.				
SO	SEQUENCE 276 AA; 10798 MW; 611FFC1222B2CC55 CRC64;				

Query Match 100.0%; Score 1466; DB 1; Length 276;
Best local similarity 100.0%; Pred. No. 6.7e-119;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MYKERSGGGGSSRSSEILGADRINDALNKKLEKSSSTTTTSKVFSSKDKDPFSFT 60

Db 1 MYKERSGGGGSSRSSEILGADRINDALNKKLEKSSSTTTTSKVFSSKDKDPFSFT 60

Oy 61 STKTQLPDVSEFTDSEGSVSGEGDTSWISWFCNLGRNDFCEVDEYIQDFNLGL 120

Db 61 STKTQLPDVSEFTDSEGSVSGEGDTSWISWFCNLGRNDFCEVDEYIQDFNLGL 120

SPECIES=MOUSE, AND PIG;
 MEDLINE; 91298153.
 RA Boldyreva B., Plontek K., Schmidt-Spaniol I., Issinger O.-J.;
 RA "The beta subunit of casein kinase II: Cloning of cDNAs from murine
 RA and porcine origin and expression of the porcine sequence as a fusion
 RA protein.";
 RL Biochim. Biophys. Acta 1068:439-442(1991).
 [8]
 RP SEQUENCE OF 4-215.
 RP SPECIES=BOVINE; TISSUE=LUNG;
 RA MEDLINE; 87260897.
 RA Takio K., Kuenzel E.A., Walsh K.A., Krebs E.G.;
 RA "Amino acid sequence of the beta subunit of bovine lung casein kinase
 RA II.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4851-4855(1987).
 [9]
 RP SEQUENCE FROM N.A.
 RP SPECIES=RABBIT;
 RA MEDLINE; 93185937.
 RA Gupta S.K., Singh J.P.;
 RA "PCR cloning and sequence of two cDNAs encoding the alpha and beta
 RA subunits of rabbit casein kinase-II.";
 RL Gene 124:287-290(1993).
 [10]
 RP SEQUENCE FROM N.A.
 RP SPECIES=RABBIT; STRAIN=NEW ZEALAND WHITE;
 RA Gupta S.K., Rothfuss K.J., Singh J.P.;
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 [11]
 RP SEQUENCE FROM N.A.
 RP SPECIES=CHICKEN;
 RA MEDLINE; 91115855.
 RA Maridov G., Park W., Krek W., Nigg E.A.;
 RA "Casein kinase II: cDNA sequences, developmental expression, and
 RA tissue distribution of mRNAs for alpha, alpha', and beta subunits of
 RA the chicken enzyme.";
 RL J. Biol. Chem. 266:2362-2368(1991).
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT.
 CC -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA' AND TWO
 CC BETA CHAINS.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN.
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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 CC
 EMBL; S56242; AAB25555.1; -
 EMBL; X16937; CAA34811.1; -
 EMBL; X16312; CAA34379.1; -
 EMBL; X57152; CAA40442.1; -
 EMBL; X80685; CAA56700.1; -
 EMBL; X30448; AAB52123.1; -
 EMBL; X52959; CAA37132.1; -
 EMBL; X56502; CAA39857.1; -
 EMBL; L15619; AAB40928.1; -
 EMBL; X56503; CAA39858.1; -
 EMBL; M98450; AAB91892.1; -
 EMBL; M59458; AAB48692.1; -
 PIR; A33554; A33554.
 PIR; A39459; A39459.
 PIR; A60651; A60651.
 PIR; C38611; C38611.
 PIR; S05016; S05016.
 PIR; S12737; S12737.
 PIR; S14478; S14478.
 PIR; S14511; S14511.
 PIR; S14724; S14724.


```

QY 263 SVVPLPFGKVVH 274
      :|::||:|:|
Db 182 QFVPRLYGFKIH 193

RESULT 9
ID KC2B_SCHPO STANDARD; PRT; 231 AA.
AC P40232;
DI 01-FEB-1995 (Rel. 31, Created)
DI 01-FEB-1995 (Rel. 31, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
GN CKBI.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94088557.
RA Rousson I., Draetta G.;
RT "The Schizosaccharomyces pombe casein kinase II alpha and beta
RT subunits: evolutionary conservation and positive role of the beta
RT subunit.";
RL Mol. Cell. Biol. 14:576-586(1994).
CC -! FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
CC -! SUBUNIT: Tetramer composed of an alpha chain, an alpha' and two
CC beta chains.
CC -! PTM: Phosphorylated by alpha chain (by similarity).
CC -! Similarity: belongs to the casein kinase 2 beta chain family.
-----
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or send an email to licensedisb@sib.ch).
-----
EMBL: X74274; CAA52330.1; --
DR INTERPRO: IPRO00704; --
DR PFAM: PF01214; CK_II_beta; 1.
DR PRINTS: PR00472; CASKNKINASFI.
DR PROSITE: PS01101; CK2_BETA; 1.
KW Transferrase; Serine/threonine-protein kinase; Phosphorylation.
SQ SEQUENCE 231 AA; 26647 MW; 2969993DA5997D28 CRC64;

Query Match 40.6%; Score 604; DB 1; Length 231;
Rest Local similarity 57.7%; Pred. No. 3.2e-44;
Matches 113; Conservative 25; Mismatches 52; Indels 6; Gaps

QY 81 SGSEFGDTS-WISWFCNLKNGNFFCEVDGYIQDDPNLCGLSGQVPYYDYALDLILDV-D 138
      ||||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 SESSESDSSQYWDPWFGLKGNEFFCEVDGFQDRFNLTGLSHVEPHYSQSJLDLILDVLD 65

QY 139 ASNSEFTQEHEWVESNAEMLVGLIHRVYLLTKGAARMTKYKNCDFGRCPVFCCGQ 198
      ||||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 PDLPFEVQDE----VVASRHLVGLIHAHYILTQAQLYKMLERYKKDFGHCPRVLCNQ 121

QY 199 SCLEPVGSQDSFRSTVKTYCPKCEDISYSPRSKPGQNDGAYGFTTFPPHIFLMTYGNLKPO 258
      ||||| |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 122 PMLPVLGSLDIAHAKSVKLXPCREDVYTPKSQRHASIDGAYGSTSFPHLMFQVYPELAVP 181

QY 259 KP-QSYVPKIFGKVH 274
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 182 KSQGVIPRTFGKVH 197

RESULT 10
ID KC2B_SPOFR STANDARD; PRT; 221 AA.

```

076485;
 15-JUL-1999 (Rel. 38, Last created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 Spodoptera frugiperda (fall armyworm).
 Cukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Ditypsia;
 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Noctuoidea; Noctuidae; Amphipyridae; Spodoptera.
 (1)
 SEQUENCE FROM N.A.
 Ebel W., Stępcowski A., Robertson N.M., Alnemri E.S., Litwack G.;
 "Identification, cloning and expression of Spodoptera frugiperda
 casein kinase II";
 Submitted (JUN-1998) to the EMBL/GenBank/CDK databases.
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF CKII ARE OBSERVED DURING
 CC EMERYGENESIS, LIVER REGENERATION, AND ADIPOCYTE DIFFERENTIATION.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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 CC
 DR EMBL; AF071211; AAC24042.1; -;
 DR INTERPRO; IPR000704; -;
 DR PFAM; PF01214; CK_II_beta; 1;
 DR PRINTS; PR00472; CASKINASE11.
 DR PROSITE; PS01101; CK2_BETA; 1.
 DR Transferrase; Serine/threonine-protein kinase; Phosphorylation.
 DR MOD_RES 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 DR DOMAIN 55 64 ASP/GIU-RICH (ACIDIC).
 DR SEQUENCE 221 AA; 25376 MW; 3317HR391D708936 CRC64;
 Query Match 39.8%; Score 592; DB 1; Length 221;
 Best Local Similarity 52.6%; Pred. No. 3.2e-43;
 Matches 101; Conservative 36; Mismatches 55; Indels 0; Gaps 0;
 Y 83 SEGDDTSWISWFCNLRGNDFCEVDEYIQDDFNLCGLSGOVYKYALDLILDVSNLS 142
 2 SSSSEVSWISWFCNLRGNDFCEVDEYIQDDFNLCGLSGOVYKYALDLILDVSNLS 61
 143 EMFTDQHEWVESAAEMLYGLIHVRYILTCKMAAMTEKYKNCDFGRCPVFCGQSLP 202
 62 LDNPQNSDLVEQASFLXGLIHARYILNRRGSGOMLEKFAQSDFGHCPVYCECCPMLP 121
 203 VGSDDTPRSTVKIYCKEDISYPRSKFGQGNIDGAYFGTTPPHLFLMTYGNLKPQKPTQ 262
 122 LGLSDVPGVAMVLYCPRCMDVYTPKSRHHHTDGAFTGTFPMVFMVHPYRPRKRPAS 181
 263 SYVVKPIFGFKVH 274
 182 QVFRLYGFKIH 193
 RESULT 11
 C22B_CAEEL STANDARD; PRI: 234 AA.
 D F28548; C62352; Q22077;
 C 01-DEC-1992 (Rel. 24, Created)
 T 01-DEC-1992 (Rel. 24, Last sequence update)
 T 15-JUL-1999 (Rel. 38, Last annotation update)
 E CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 N KIN-5 OR KIN-10 OR T01G9.6.
 N Caenorhabditis elegans.
 C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 C Rhabditidae; Telodoridae; Caenorhabditis.

RP SEQUENCE FROM N.A.
 RP MEDLINE: 92011787.
 RA Hu E., Rubin C.S.;
 RT "Casein kinase II from Caenorhabditis elegans. Cloning,
 RT characterization, and developmental regulation of the gene encoding
 RT the beta subunit";
 RL J. Biol. Chem. 266:19796-19802(1991).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Lennard N.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/UDRJ databases.
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF CKII ARE OBSERVED DURING
 CC EMERYGENESIS, LIVER REGENERATION, AND ADIPOCYTE DIFFERENTIATION.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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 DR EMBL; M73827; AAA27963.1; -;
 DR EMBL; Z75713; CAB00056.1; -;
 DR EMBL; Z75713; CAB00053.1; -;
 DR PIR; A41036; A41036.
 DR WORMPEP; T0169.6A; CE18168.
 DR WORMPEP; T0169.6B; CE06343.
 DR INTERPRO; IPR000704; -;
 DR PFAM; PF01214; CK_II_beta; 1.
 DR PRINTS; PR00472; CASKINASE11.
 DR PROSITE; PS01101; CK2_BETA; 1.
 DR Transferrase; Serine/threonine-protein kinase; Phosphorylation;
 KW Alternative splicing.
 KW MOD_RES 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 FT DOMAIN 55 63 ASP/GIU-RICH (ACIDIC).
 FT VARSPLIC 58 58 P -> PE (IN ISOFORM B).
 FT CONFLICT 141 141 M -> D (IN REF. 2).
 SQ SEQUENCE 234 AA; 26452 MW; A0814A48B768347D CRC64;
 Query Match 39.6%; Score 588.5; DB 1; Length 234;
 Best Local Similarity 53.3%; Pred. No. 6.7e-43;
 Matches 104; Conservative 36; Mismatches 48; Indels 7; Gaps 2;
 QY 83 SEGDDTSWISWFCNLRGNDFCEVDEYIQDDFNLCGLSGOVYKYALDLILDV---DA 139
 2 SSSSEVSWISWFCNLRGNDFCEVDEYIQDDFNLCGLSGOVYKYALDLILDV---DA 61
 QY 140 SENSEFTDQHEWVESAAEMLYGLIHVRYILTCKMAAMTEKYKNCDFGRCPVFCGQSLP 199
 62 EDNAINTD-----LVEQAAEMLYGLIHARYILNRRGSGOMLEKFAQSDFGHCPVYCECCPMLP 117
 QY 200 CLPVGQSDTPRSTVKIYCKEDISYPRSKFGQGNIDGAYFGTTPPHLFLMTYGNLKPQK 259
 118 MLPGLSDVPGVAMVLYCPRCMDVYTPKSRHHHTDGAFTGTFPMVFMVHPYRPRKRPAS 177
 QY 260 PTQSYVVKPIFGFKVH 274
 178 PVTQVVKLYGFKIH 192
 RESULT 12
 KC2C_DROME STANDARD; PRI: 219 AA.
 ID KC2C_DROME
 AC Q96863; Q9V919;

15-JUL-1999 (Rel. 38, Created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 01-OCT-2000 (Rel. 40, Last annotation update)
 CASEIN KINASE II BETA' CHAIN (CK II) (EC 2.7.1.37).
 CKII-BETA2.
 Drosophila melanogaster (fruit fly).
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 [1]
 SEQUENCE FROM N.A.
 Bidwai A.P., Zhao W., Glover C.V.C.;
 "A gene located at 56F1-2 in *Drosophila melanogaster* encodes a novel
 metazoan beta-like subunit of casein kinase II";
 Mol. Cell Biol. Res. Commun. 1:21-28(1999).
 [2]
 SEQUENCE FROM N.A.
 STRAIN-BERKELEY;
 MEDLINE: 20196006.
 Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gorayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Hest G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boishakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattler P.,
 Hurlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 Foster C., Gabriele A.E., Garg N.S., Gelbart W.M., Glessner K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison C.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip C., Lai Z.,
 Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson P.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy R., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Steden-Kamos I., Simpson M., Skupski M.P., Smith I.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
 Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao C., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter C.C.;
 "The genome sequence of *Drosophila melanogaster*";
 Science 287:2185-2195(2000).
 [3]
 FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT.
 [4]
 SUBUNIT: TRIMER OF TWO ALPHA AND TWO BETA' CHAINS.
 [5]
 PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 [6]
 SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA' CHAIN FAMILY.
 [7]
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 or send an email to license@isb-sib.ch).
 [8]
 EMBL; U51209; AA000080.1;
 EMBL; AE003792; AAF57483.1;
 [9]
 FLYBASE: FBgn0026136; CKII-Beta2.
 INTERPRO: IP0000704;
 PFAM: PF01214; CK_II_beta; 1;
 PRINTS: PRO0472; CASRKINASEII.
 PROSITE: PS01101; CK2_BETA; 1;
 TRANSFERASE: Serine/threonine-protein kinase; Phosphorylation;
 MOL.MES 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 DOMAIN 63 71 ASP/GLU-RICH (ACIDIC).
 SEQUENCE 219 AA; 24966 MW; E43E80AA465DB666 CRC64;
 Query Match 36.2%; Score 538; DB 1; Length 219;
 Best Local Similarity 48.4%; Pred. No. 1.2e-38;
 Matches 93; Conservative 37; Mismatches 60; Indels 2; Gaps 2;
 QY 83 SEGDDTSWISWFCNLKGNDFCEVDEYQDDNFNLGSLGQVPPYYALDILDVDASNS 142
 DB 2 TDSDESSIIHWFCKQRNEFFCEVDEYQDDNFNLGSLGQVPPYYALDILDVDASNS 61
 QY 143 EMFTDQEHMVESAEMLYGLIHVRYLTITKGNAAATEKYKNCDFGCRVFCGSGSLP 202
 DB 62 S--EDPAEPLEASAKLYGLIHARFILNRGIELMDKYNGKGFCTCFACFUSQVLP 115
 QY 203 VGSDDIPRSSTVVIYCPKCEDISYPSKFGNIDGAGFYGTFPHLFLMTYGNLKPQKPTQ 262
 DB 120 IGLSDNFEGDMVRIYCPKNDVYIPKASRHSNLDGAFGTFGPHMFMEKPDARPKRAQ 179
 QY 263 SYVPKTFGPKVH 274
 DB 180 KVPRLYGFKEIH 191
 RESULT 13
 KC2C_YEAST STANDARD; PRT: 258 AA.
 AC P38930;
 DI 01-FEB-1995 (Rel. 31, Created)
 DI 01-FEB-1995 (Rel. 31, Last sequence update)
 DI 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA' CHAIN (CK II) (EC 2.7.1.37).
 GN CKB2 OR YOR039W OR OR26.32.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94299539.
 RA Reed J.C., Bidwai A.P., Glover C.V.C.;
 "Cloning and disruption of CKB2, the gene encoding the 32-kDa
 regulatory beta'-subunit of Saccharomyces cerevisiae casein kinase
 II";
 J. Biol. Chem. 269:18192-18200(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC S-KIN-S288C / FY1679;
 RA de Haan M., Mease A.C., Grivell L.A.;
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 172-258 FROM N.A.
 RC STRAIN-AP3;
 RA Haider M., Bito A., Wallner J., Breitenbach M.;
 Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP PARTIAL SEQUENCE.
 RX MEDLINE: 94182950.
 RA Bidwai A.P., Reed J.C., Glover C.V.C.;
 "Casein kinase II of Saccharomyces cerevisiae contains two distinct
 regulatory subunits, beta and beta'";
 Arch. Biochem. Biophys. 309:348-355(1994).
 RL

-!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE
 BETA CHAIN AND ONE BETA' CHAIN.
 -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 -!- PTM: THE N-TERMINUS IS BLOCKED.
 -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.

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EMBL: U08849; AA21656.1;
 EMBL: X87331; CAA60758.1;
 EMBL: Z74947; CAA59229.1;
 EMBL: X82893; CAA58064.1;
 SGD: S0005565; CKR2.
 INTERPRO: IPR000704;
 Pfam: PF01214; CK_II_beta.1.
 PRINTS: PR00472; CASNKINASEII.
 PROSITE: PS01101; CK2_BETA.1.
 Transferrase: Serine/threonine-protein kinase; Phosphorylation.
 SEQUENCE 258 AA: 29842 MW: D6060CB3C70B19A4 CRC64:

Query Match 34.6%; Score 514.5; DB 1; Length 258;
 Best Local Similarity 46.0%; Pred. No. 1.4e-36;
 Matches 99; Conservative 35; Mismatches 74; Indels 7; Gaps 2;
 62 TKQLPDVSESDSGSSGEGDFTISNFCNLKNGDCEVDEVIQDQFNLCGLS 121
 16 SRVQGVVLMDDSDSEV-----DWKIDIFLGRKGHEVFCDDVPEYITDRENLNNQ 69
 122 GQVPPVYVYALDII--DVDASNSIMFTDEQHEVSAEMVGLIRVYIILTKGMAANPE 180
 70 KTVSKESYVYVIVDLDSDSIENWTHALEQENSSKLYGLIHKRYII--KGLQKMYA 129
 181 KYKNCFDGRCPVFCGQSCFLVGSQDIPRSSTVKIYCPKCEDISYPSKPGQNGIDGYF 240
 130 KYKADFGRCRVYCNLOOLVGLHDLPGIDCVKLYCSQEDIAIYPSKSRSSIDGYF 189
 241 GTTFPHLEMTGNLKPQKPTGQSYVZPKIEGFVHK 275
 190 G-SFGPMFLQAPPMVPRKPTKRYVPRKIFGFLHK 224

RESULT 14
 22B_YEAST
 KC2B_CANAL STANDARD; PRT; 278 AA.
 AC G59906;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 GN CKB1 CR YGLO15W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RP SEQUENCE FROM N.A.
 RA STRAIN=S288C;
 MEDLINE: 93256195.
 AB Bidwai A.P., Reed J.C., Glover C.V.C.;
 "Cloning and disruption of CKB1, the gene encoding the 38-kDa beta
 subunit of Saccharomyces cerevisiae casein kinase II (CKII). Deletion
 of CKII regulatory subunits elicits a salt-sensitive phenotype".
 J. Biol. Chem. 270:10395-10404(1995).
 [2]
 SEQUENCE FROM N.A.

RA Hebling U., Hofmann B., Delius H.;
 Submitted (May-1996) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE
 BETA CHAIN AND ONE BETA' CHAIN.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.

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 or send an email to license@isb-sib.ch).

EMBL: U21283; AAA86829.1;
 EMBL: Z72541; CAA96719.1;
 SGD: S0002987; CKB1.
 INTERPRO: IPR000704;
 Pfam: PF01214; CK_II_beta.1.
 PRINTS: PR00472; CASNKINASEII.
 PROSITE: PS01101; CK2_BETA.1.
 Transferrase: Serine/threonine-protein kinase; Phosphorylation.
 SEQUENCE 278 AA: 32265 MW: 9ACABD285E6990AF CRC64:

Query Match 30.3%; Score 446; DB 1; Length 278;
 Best Local Similarity 38.4%; Pred. No. 9.5e-31;
 Matches 69; Conservative 47; Mismatches 58; Indels 38; Gaps 4;
 QY 81 SGSEGGDFTISNFCNLKNGDCEVDEVIQDQFNLCGLSGQVYDYALDIL 135
 DB 12 TGSDDSSGAYDEWIPSCSRFGHEVFCQVTFIEDDFNMTLSLQEVPIRYKALDIL 71
 QY 136 DVDAS-----NSPMFTDEQHE-----MVESAAEMLYGLIH 165
 DB 72 DLEANSDEEDEDVDEVDQENQSDGDEGRNKRSPVNVKSIIEHRAEQLYGLIH 131
 QY 166 VRYLTITKGMAEMTKYKNCDFGRCPVFCGQSCFLVGSQDIPRSSTVKIYCPKCEDIS 225
 DB 142 ARFILLTKPCLQAMAEKFDHKEFGTCPRYCNQMOILPGCLSDITVGHKTVRLYCPSCQDLY 191
 QY 226 YPSKFCQNGIDGAVFGITFPHLEMTGNLKPQKPTGQSYVZPKIEGFVHK 274
 DB 192 LPQSSRFCLLEGAFWGTSPGVFLKHFKELEEVYVERKSKESTELKVFGRIN 243

RESULT 15
 KC2B_CANAL STANDARD; PRT; 294 AA.
 AC G59906;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 GN CKB1.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC anamorphic Saccharomycetales; Candida.
 RP SEQUENCE FROM N.A.
 RA Waiz K., Pardo P.S., Passeron S.;
 "Complete sequence of the protein kinase CK2 beta subunit gene from
 Candida albicans (CaCKB1)".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RP CHARACTERIZATION
 RC STRAIN=ATCC 64385 / i001;
 RX MEDLINE: 97288362.
 RA Waiz K., Pardo P.S., Passeron S.;
 "Purification and characterization of protein kinase CK2 from Candida

```

albacans: evidence for the presence of two distinct regulatory
subunits beta and beta.":
Arch. Biochem. Biophys. 343:347-354(1997).
-- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
-- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one
beta chain and one beta' chain.
-- PTM: PHOSPHORYLATED BY ALPHA CHAIN.
-- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL: AF036546; AAC15240.1; -
INTERPRO: IPR000704;
PFAM: PF01214; CK II beta; 1.
PRINTS: PR00472; CASEKTNASH.1.
PROSITE: PS0110; CK2_BETA; 1.
Transferrase: Serine/threonine-protein kinase; Phosphorylation.
SEQUENCE 294 AA; 33800 MW; 0592F6BC59FC3309 CRC64;

```

Arch. Biochem. Biophys. 349:347-354 (1997).

-1- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).

-1- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE BETA CHAIN AND ONE BETA' CHAIN.

- ! - PTM: PHOSPHORYLATED BY ALPHA CHAIN.

-!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.

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EMBL: AF036556; AAC15240.1; -
INTERPRO: IPR000704; -
PFAM: PF01214; CK_II_beta: 1,
PROSITE: PRO0472; CASPKINASE1;
PROSITE: PCS110; CK2_BETA;
Transferrase: Serine/threonine-protein kinase; Phosphorylation;
SEQUENCE 294 AA; 3380 MW; 0592F6B059FC309 CRC64;

EMBL; AF036546; AAC15240.1; -.

INTERPRO: IPROC0704; - -

PFAM; PF01214; CK_II_beta; 1.

PRINTS; PRO0472; CASNKINAS:!!.

PROSITE: PSC110; CK2_BETA; ...

Transferase; Serine/threonine-protein kinase; phosphorylation.

SEQUENCE 294 AA; 33800 MW; 0592F8BC59FC33C9 CRC64;

Query Match 29.9%; Score 445; DB 1; Length 294;
Best Local Similarity 40.5%; Pred. No. 1.2e-30;
Matches 92; Conservative 35; Mismatches 68; Indels 32; Gaps 4;

Best Local Similarity 40.58; Pred. No. 1.2e-30;

Matches 92; Conservative 35; Mismatches 68; Indels 32; Gaps 4;

81 SGSEGDDT\$WISWFCNLRGNDFCEVDEYIQDDFNLCGI.SGQVPYYDYALDILLDVDAS 140

3 SDPEEDYIPWIIQQLCELFGHGYFVQVSQFIEDDFNL.TCLSSQVPYYREALYTLJDYQVE 62

141 NSEMF-TDE-----QHEMVESAEMLYGLIHVRYILTTKGM 175

[illegible]

63 TAEDHNTDNTTNTSNNDSRNGTSKRNASL_PNKALLAHSAELLYGJHARYIVSKQGL 122

176 AAMTEKYKNCDFGRCPRVFCCQSCI.PVGCSLPRSTVKIYCPKCHISYPRSKFQGN1 235

1123 TAMASKFERNDFGSCPRYFCDGMHILIPVGSTDPGQETVRLFCPCNDIYPSSRYLNI 182

236 DGAYFGTTFPHLFLMYGNLKPQ-----KPTQS-YVPKIFGFKVHK 275

[illegible]

183 DCAFFCTTFPGLLVKMFPEIENQCRIRI LKFSQND:GLKLFCKINE 225

arch completed: November 15, 2000, 13:29:35

b time: 315 sec

GenCore version 4.5
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M nucleic - nucleic search, using sw mode.
Run on: November 15, 2000, 11:23:49 : Search time 1249.31 Seconds
(without alignments)
3775.673 Million cell updates/sec
Title: us-09-359-026-1
Perfect score: 1080
Sequence: t gtcgaccacgcgtccgaga.....tggagcatacatcaaacatt 1880
Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 2.0
Searched: 1033670 seqs, 2183789503 residues 2057340
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenBank:
1: gb_ba1:
2: gb_ba2:
3: gb_cm:
4: gb_ov:
5: gb_pat:
6: gb_ph:
7: gb_pl1:
8: gb_pl2:
9: gb_pl3:
10: gb_pr2:
11: gb_pr3:
12: gb_ro:
13: gb_sy:
14: gb_un:
15: em_fun:
16: em_hum1:
17: em_hum2:
18: em_in:
19: em_or:
20: em_ov:
21: em_ov:
22: em_pat:
23: em_ph:
24: em_pl:
25: em_ro:
26: em_sy:
27: em_sy:
28: em_un:
29: em_vil:
30: gb_ba1:
31: gb_in1:
32: gb_in2:
33: gb_in3:
34: gb_pl3:
35: gb_pl4:
36: em_bal:
37: em_ba2:
38: em_htg1:
39: em_htg2:
40: em_htg3:
41: em_htg4:
42: em_htg5:
43: em_htg6:

- 44: em_htg7:
45: em_htg8:
46: em_htg9:
47: em_htg10:
48: em_htg11:
49: em_htg12:
50: em_htg13:
51: em_htg14:
52: em_htg15:
53: em_htg16:
54: em_htg17:
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56: em_htg19:
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63: em_hum5:
64: em_hum6:
65: gb_pr5:
66: gb_pr6:
67: gb_pr7:
68: gb_htg:
69: gb_htg2:
70: gb_htg3:
71: gb_htg4:
72: gb_htg5:
73: gb_htg6:
74: gb_htg7:
75: gb_htg8:
76: gb_htg9:
77: gb_htg10:
78: gb_htg11:
79: gb_htg12:
80: gb_htg13:
81: gb_htg14:
82: gb_htg15:
83: gb_htg16:
84: gb_htg17:
85: gb_htg18:
86: gb_htg19:
87: gb_htg20:
88: gb_htg21:
89: gb_htg22:
90: gb_htg23:
91: gb_sts1:
92: gb_sts2:
93: gb_vil:
94: gb_vil2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1080	100.0	1080	7	AF068318 Arabidops
2	605	56.0	88548	6	AF068318 Arabidops
3	591.4	54.8	10989	7	AF263518 Arabidops
4	413.2	38.3	1285	8	ATHCKIB Arabidops
5	390.6	36.2	1229	8	AF003984 Arabidops
6	245.6	22.7	66033	7	AC003672 Arabidops
7	264.4	18.9	648	4	XLCKIIB Arabidops
8	201.2	18.6	1677	4	S76877 casein kina
9	198	18.3	1645	4	AF133088 Cyprinus
10	183	16.9	914	12	MMCKIIB Mouse mRNA
11	183	16.9	944	12	MMCKIIB Mouse CK11
12	182	16.9	521	66	HSCK11 Human mRNA


```

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1 (bases 1 to 10989)
Browning, K.S. and Wong, K.
Unpublished
2 (bases 1 to 10989)
Browning, K.S. and Wong, K.
Direct Submission
AUTHORS Submitted (03-MAY-2000) Chemistry & Biochemistry, University of
JOURNAL Texas at Austin, Austin, TX 78712, USA
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We thank the CSHL/Mashu/ARI consortium for sequencing RAC clones F6P23, F5J6, I17A9, and T13J26, the ESSA group for sequencing clone F1304, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Iabata for helpful assistance. In addition, we would like to thank the IIGR Bioinformatics Department, especially Lixi Zhou, Hanif Khaliq, Michael E. Reaney, Lily Fu, Peng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

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Address all correspondence to: atetigr.org.

FEATURES

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y 440 atgatlctctctgtgaagtcgagatgaatttatattcaagatgatttcaactcttttgtggtt 459
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b 42564 ATGAGTTTTTCTGTGAAGTAGATGAGAAATATATAACAAGATGANTTCAATCTCTGTGGTI 42505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
y 500 taagtgtcgaagcccctactatgattatgacctgactgactcaatttaagtattgaatctt 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 42504 TGAGTGTCTCAAGTTCCTCTACTATGATTAATGCACTTGATCTCAITTTAGATGTGTAATCAI 42445
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y 560 ccaacacatgag----- 570
    || | || | || | || | || | || | || | || | || | || | || | || | || | || |
b 42444 CAAATGCTAGTCGACGGTCCATTTTCAIGAAATTAAGTCTTACTTTCTCTCAGCAATTCIT 42385
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y 571 -----abgttactgatgaacagcatgaa 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 42384 GTATAATTTGGAGGAATGTTTATTTGGATAGGTGATGATGTTTACTTGAAGAACATCATGAG 42325
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Qy	595	atgtggaaatcagctgtgagatgctatagttcttattcatgttcglaacaatttgaact	654
Db	48324	ATGTGGAAATCAGCTGTCGAGATGTTATATGCTTATTCATGTTGCTTATATTCCTACT	48265
Qy	655	actaaagaataggctgcaat-----	674
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Qy	675	-----gactgagaagtacaagaactgtgatttcgg	704
Db	48204	ATCTTTGAATCATATCTTCTCTTTTGTAGATGGAGAAGTATAGAAATTAATGATTTCGG	48145
Qy	705	gagatgccccgagaattttctgttcggtgcadtcttcttcgaattgacaaatccgataa	764
Db	48144	CAGATGCCCCAGAGAGTTTCTCTGTCGGGACAGCTGTGCTCCGGTTCGCCAATCTGATAT	48085
Qy	765	cccagatccgaactgtgaagataaactgcccaaatgcagagatatattcttaccacg	824
Db	48084	CCCGAGGTCGAGCACTGTGAAGATATATCGCCAAAATGCGAGAGATATTACTACCCGCG	48025
Qy	825	atctaaattccaaagccaattatgtaggagctactttggaaaccacatt	872
Db	48024	ATCTAAATACCAAGGCAGTATCCTTIGTCTCTCTCTCAAAAAGCIT	47977
RESULT	7		
X:CKLIIB		648 bp mRNA	VRT 07-APR-1992
LOCUS		X laevis mRNA for beta subunit of casein kinase II.	
DEFINITION		X62376	
ACCESSION		X62376.1	
VERSION		GI:64529	
KEYWORDS		casein kinase; casein kinase II beta subunit; casein kinase-II; ser/thr protein kinase.	
SEARCH		African clawed frog.	
ORGANISM		Xenopus laevis	
REFERENCE		Eukaryota; Melarzoa; Chordata; Vertebrata; Amphibia; Batrachia;	
AUTHORS		Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.	
TITLE		1 (bases 1 to 648)	
JOURNAL		Allende,J.E.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (10-DEC-1991) J.E. Allende, Facultad de Medicina, Civ.	
TITLE		Cs. Medicas Norte, Dept. de Bioquimica, Univ. de Chile,	
JOURNAL		Independencia 1027, Casilla 70086, Santiago 7, CHILE	
REFERENCE		2 (bases 1 to 648)	
AUTHORS		Jedlicki,A., Hinrichs,M.V., Allende,C.C. and Allende,J.F.	
TITLE		The cDNAs coding for the alpha- and beta-subunits of Xenopus laevis	
JOURNAL		casein kinase II	
MEDLINE		FEBS Lett. 297 (3), 280-284 (1992)	
COMMENT		92183611	
FEATURES		See also X62375.	
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		HYRALDMILDLEDELEEDNPNSDLIEQAAEMLYGLIHARYILTRNGIAQMLEKVG	
		QDGYGCPVYCEKNQPMPLGLSDIPGEMAVKLCFKPMQMDVITPKSRHHHTDGAIFG	
		TGTFPHMVPHEPRKRPANQFPRLYGFKIHFMAYOLQQAASNFKSPVKTMR	
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BASE COUNT			
ORIGIN			

[illegible]

46. .693
/gene="casein kinase 2 beta subunit, CK2 beta"


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REFERENCE      1 (bases 1 to 1645)
AUTHORS       Vera,M.I., Kausel,G., Barrera,R., Leal,S., Figueroa,J. and
               Quezada,C.
TITLE         Seasonal adaptation modulates the expression of the protein kinase
               CK2 b subunit gene in the carp
JOURNAL       Biochem. Biophys. Res. Commun. (2000) In press
REFERENCE     2 (bases 1 to 1645)
AUTHORS       Vera,M.I., Kausel,G. and Barrera,R.
TITLE         Direct Submission
JOURNAL       Submitted (04-MAR-1999) Instituto de Bioquímica, Universidad
               Austral de Chile, Casilla 567, Valdivia, Decima Region 00000, Chile
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               /issue_type="liver"
  CDS         34..1681
               /gene="CK2-b"
               /codon_start=1
               /product="CK2 beta subunit"
               /protein_id="AAF66446.1"
               /db_xref="GI:7672553"
               /translation="MSSSEVSWSWFCOLRGNEFFCVDVEDYIQDKFNLTGLNHOVP
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               QGDFGCPVYVCENQPMPLIGLSIDPGEMVLYCPKCMVDVTPKSRHHHTDGNVFG
               TGFPHLMFVHPEYRPRRPAQFVPRLYGFKLHPAYQCLQAASFKSPVKTR"
  BASE COUNT  447 a 351 c 371 g 476 t
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Query Match      18.3%; Score 198; DB 4; Length 1645;
Best Local Similarity 58.8%; Pred. No. 5.3e-39;
Matches 342; Conservative 0; Mismatches 240; Indels 0; Gaps 0;
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46 GAGGAAGTCTGGTGAATCTTGTTGGTCTACGGAGGCTGAGACGATCTCTCGGAG 105
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457 qtcgatgaagattattcaagatgatttcaattcttcttgaatttgaagatgaagtcct 516
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106 GAGATGAGAGTACATCAGGACAAATTCATCTTACGGACTCAATGAGGAAGTTCOC 165
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517 taatgattatgaactgaactgaactatagatgattgaacttccacaaatgaagatt 576
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166 CATTACAGACAGCCCTGGACATGATCTGGATCTGGACCTGATGAGGAGCTGGAGGAC 225
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577 actgatacagacatgaatgttggaatcagctgtcagatgctatattctattctat 636
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225 AACCTAACCGAGTACCTGATGAGGAGGCTGCTGAGATGCTGTATGAGATGATCCAT 285
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637 gtlcqtatcaltttagactactaaagaagaatggcttgcatactgaatgagaagtaactgt 696
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286 GCGCGCTACATCTCTACTACCTGCGCATTCGCCAGATGCTGAGAGAATACCAGCAGGGA 345
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697 gatttcggagagagagcagagatttcttcttgcgggtcaactcttgcattccag; 756
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346 GNTTTTGGCTATTGTTCTCTGTTTACTGTGAGAAATACGCAATGCTGGCCATTGGGCTC 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
757 tccgatatcccgagatcgagactgtgaagatactatctgctcaaatgcgaggaatatct 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
406 TCTGACATCTCTGGCGAGGCGCATGGTGAGCTACTGCGCTTAAGTGTATGATGTGTAC 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
817 tacccgcgatctaaattccaaaggaatatttgatgagcgtgaactttgaaaccacattccct 876
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
466 ACACCCAAAGTCCTCCAGGCCACCATCACCGATGAGGCTGATTTTGGCACTGCTTCCOC 925
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877 caattgtcttgaacttaacggaacttaaacccgcagagaagcactactcaaaactatgac 936
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526 CAGATGCTCTTCAATGTGATGTCCTGTAGTACGCGCAAGAGGCGTCCACACCAAGTTTGTG 985
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937 ccaaaaactcttggcttcaaggttacacaaaccatgatactag 978

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586 CCACGGCTCTATGTTTCAAGATTACCCCAAGGCTTACCAG 627

RESULT 10
LOCUS      MMCK11B          914 bp      mRNA      ROD      12-SEP-1993
DEFINITION Mouse mRNA for casein kinase II beta subunit (EC 2.7.1.37).
ACCESSION X52959
VERSION   X52959.1 GI:50418
KEYWORDS  casein kinase; protein kinase.
SOURCE     house mouse
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 914)
            Direct Submission
            Submitted (07-MAY-1990) Canaani D., Tel Aviv University, Department
            of Biochemistry, Tel Aviv University, Tel Aviv 69978, Israel
REFERENCE 2 (bases 1 to 914)
            Kopatz,I., Naiman,T., Eli,D. and Canaani,D.
            The nucleotide sequence of the mouse cDNA encoding the beta subunit
            of casein kinase II
            Nucleic Acids Res. 18 (12), 3639 (1990)
            Data kindly reviewed (27-AUG-1993) by Canaani D.
FEATURES
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               /db_xref="SWISS-PROT:P13862"
               /translation="MSSSEVSWISWFCOLRGNEFFCVDVEDYIQDKFNLTGLNHOVP
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               QGDFGCPVYVCENQPMPLIGLSIDPGEMVLYCPKCMVDVTPKSRHHHTDGNVFG
               TGFPHLMFVHPEYRPRRPAQFVPRLYGFKLHPAYQCLQAASFKSPVKTR"
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Best Local Similarity 57.7%; Pred. No. 2.9e-35;
Matches 327; Conservative 0; Mismatches 240; Indels 0; Gaps 0;
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139 TGAGGAGGTCCTGGATTCCTGTTCTGTGGGCTCCGTGGTATGATGATCTCTGTGA 198
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456 agtcgaagaagattatltcaagatgatttcaactcttctgtgtttaaagtgtcaagtcct 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 GGTGGATGAAGACTACATCCAGGACAAATTTAATCTTACTGGACATCAATGACGAGTGC 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
516 ttaactatgattatgaactgaacttattttagatgtttagatgttcccaacagtgaatt 575
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259 TCACATATGACAAAGCTCTGGACATGATCTTAGACCTGGAACCTGATGAAGAGCTGGAGA 318
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576 tactgatgaacagatgaatggttgaatcagctgctgagatgctatattctatttacc 635
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319 CAACCCCAACCCAGACGACCTGATGACAGCAGCTGAGATGCTTTATGGTTGATCCCA 378
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379 CCGCCGCTACATCCTCACCACCGAGGATCGCACAAATGTTGGAAAGTACCAGCAGGG 438

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459 TTCACATATCCAGAGCGAGGCTATGSGTGAAGCTCTACTGCCCAAGTCATGACGTGTA 558
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816 ttaccctcgatctataattccgagggcaattttatgagagatatttttgaacccacattccc 875
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559 CACACCCGANGTCTCCAGACACACACACACGAGGCGGCTACTCTGCCATGTGTTTCC 618
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876 tcaattgtctcttgagagacttaccgggaacttaccgagcgaggaacctattaccgaagctatg 935
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619 TCACATGCTCTTCATGTGTGATCCAGAGTATCCGCGCCCAAGCGACCTGCCCAACGAGTTTGT 678
|||||
936 ccccaaaatcttggcttccaaggtaca 962
|||||
679 NCCACGGCTCTNTGCTTCAANGATCCA 705

SUJ 11
 CILBIM
 CUS
 FNITION
 CESSION
 RSION
 YMODS
 UCE
 ORGANISM
 MUS MUSCULUS
 EUKARYOTA: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 944)
 Boldyreff, B.
 Direct Submission
 Submitted (08-NOV-1990); B. Boldyreff, INSTITUT F HUMANGENETIK,
 UNIVERSITAET DES SAARLANDES, D-6650 HOMBURG
 2 (bases 1 to 944)
 Boldyreff, B., Plontek, K., Schmidt-Spaniol, I. and Issinger, O.G.
 The beta subunit of casein kinase II: cloning of cDNAs from mu-
 and porcine origin and expression of the porcine sequence as a
 fusion protein
 Biochim. Biophys. Acta 1088 (3): 439-441 (1991)
 91198753
 MEDLINE

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FEATURES             Location/Qualifiers
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     SE COUNT          249 a 264 c 215 q 216 t
     IG_N              16.9%; Score 163; EH 12; Length 944;
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                        Matches 327; Conservative 0; Mismatches 240; Indels 0; Gaps

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[illegible]

RESULT 12

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HCKII
LOCUS       921 bp      mRNA      PRI      12-SEP-1993
DEFINITION Human mRNA for phospho(vin)/casein kinase II beta subunit.
ACCESSION   X16312
VERSION     X16312.1  GI:29964
KEYWORDS    casein kinase II; phosvitin.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euthoria;
             Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 921)
AUTHORS     Jakobi R., Voss H. and Pyerin, W.
TITLE       Human phospho(vin)/casein kinase type II. Molecular cloning and
             sequencing of full-length cDNA encoding subunit beta
             Fur. J. Biochem. 183 (1), 227-233 (1989)
JOURNAL     89325340
COMMENTS   Data kindly reviewed (26-OCT-1989) by Jacobi R.
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             CDS

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Best Local Similarity		57.7%	Pred. No. 2.9e-35;		
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CKLIB
CUS      SPCK118      837 bp      mRNA      PLN      27-JAN-1994
FINITION  S.pombe mRNA for casein kinase II beta subunit.
CESSION   X74274
VERSION   X74274.1 GI:452289
WORDS     casein kinase II; casein kinase II beta subunit.
ORIGIN    fission yeast.
ORGANISM  Schizosaccharomyces pombe
          Eukaryota; Fungi; Ascomycota; Ascomycetes;
          Schizosaccharomycetales; Schizosaccharomycetaceae;
          Schizosaccharomyces.
          1 (bases 1 to 837)
          Direct Submission
          Submitted (23-JUL-1993) I. Roussou, EMBL, Differentiation
          Programme, Meyerhof-Strasse 1, 69117 Heidelberg, FRG
          2 (bases 1 to 837)
          Roussou, I. and Prætorius, G.
          The Schizosaccharomyces pombe casein kinase II alpha and beta
          subunits: evolutionary conservation and positive role of the beta
          subunit
          Mol. Cell. Biol. 14 (1), 576-586 (1994)
          94088557
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              /clone_lib="ZAPII S.pombe cDNA"
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          SE COUNT      261 a 165 c 161 g 250 t
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Query Match      16.8%; Score 181.4; D8 34; Length 837;
Best Local Similarity 58.8%; Pred. No. 7.2e-35;
Matches 336; Conservative 0; Mismatches 226; Indels 9; Gaps 1;

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91  GATGATCTCAATATTCGCTGATCGTTTACGACTAAAAGGAACGATTTTTCG 150
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454  gaatgatgaagattatattcaagatgatttcaatcttctgtgttgaatggtaacgtc 513
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151  GAAGTCGAGAGACTTCACGAGTCCGTTTAAATTTGACTGGATTGAGTCATCAAGTT 210
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
514  ccttactatgatctatgcattgatctcattctagatgttgatgttcccaatgtagatg 573
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211  CCACACTACCTCCAGTCCTTACACCCCTATTTAGATGTATTGGATCCGCA----- 261
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574  ttctatgatgaacagcatgaatggttggagatcagctgagatgctatatactcttatt 633
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
262  TTACACAGAGAACACACAGATGAGGTAGAGGACTGCTCCTCATTTGTACGGCTTAT 321
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634  catgttgcatttcttactaagaagaatgggtgcattgactgagagtaagaagac 693
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322  CAGGCCCGTTATATCTTAAGGCTCAGCTTATATAAATGCTTGAGAAATACAAAAA 381
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
694  tggatttcggagagacccgagaggtttctcttgcgttcagctcttgccttccattgga 753
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

382  TGTGACTTTGGCAATGCCCIAGAGTTTATCCACAGCAGACGCCCAATGTTGCCCGTCGGC 441
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
754  caatccgatatcccgagatcgagtaactgtgaagatatactgccttaaaatgagagata 813
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
442  TTTCGGATATTGCCCATCAAAATCCGTTAAATATATCTGCTCGGTGTGAGGATGTG 501
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
814  tcttaccgcgagatctcaattccaggcaattattgatggagctactttggaaacacattc 873
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
502  TAGACACCAAAATACAGAGACATCATCCATGATGGTGCATATTTTGGAAACCTCATTC 561
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
874  cctcactgttcttgatgacttacgggaacttaagccgcagagacccctactcaaaagctat 933
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
562  GCTCACTAGCTTTTTCAGGTATACCTGACCTGACCTGCGTCCCTAAATCTCAAGAACGCTAC 621
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
934  gccccaaaacttttgcttgccttcaaggtatcacca 964
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
622  ATTCCACGATATTTTTGGTTTCAAGTACATA 652

RESULT 15
RATCK2BETA
LOCUS      RATCK2BETA      1964 bp      mRNA      ROD      18-FEB-1994
DEFINITION Rat casein kinase II beta subunit (CK2) mRNA, complete cds.
ACCESSION   U55619
VERSION     U55619.1 GI:415717
KEYWORDS    casein kinase II beta subunit.
SOURCE      Rattus norvegicus (library: lambda q11) liver cDNA to mRNA.
ORGANISM    Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
          1 (bases 1 to 1964)
          Ahmed, K., Davis, A., Hanlen, J., Lambert, D., McIvor, R.S. and
          Goueli, S.A.
          Cloning of cDNAs encoding the alpha and beta subunits of rat casein
          kinase 2 (CK-2): Investigation of molecular regulation of CK-2 by
          androgens in rat ventral prostate
          Cell. Mol. Biol. Res. 39, 451-462 (1993)
          94227842
          Location/Qualifiers
            1..1964
              /organism="Rattus norvegicus"
              /db_xref="taxon:10116"
              /tissue_type="liver"
              /tissue_lib="lambda q11"
              114..1930
                /gene="CK2"
                114..761
                  /gene="CK2"
                  /codon_start=1
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                  /protein_id="AAA40928.1"
                  /db_xref="GI:415718"
                  /translation="MSSSEVSWISWFCGLRNCNFFCEVDEUYIQDKNLTGLNEQVP
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                  TGFPHLPMVHPYRKRPNQFVPRLYGFIHPMAYQLQQAASNEKSPVKTI"
              876..881
                /polyA_signal
                /gene="CK2"
                1456..1461
                  /polyA_signal
                  /gene="CK2"
                1737..1742
                  /polyA_signal
                  /gene="CK2"
                1925..1930
                  /polyA_signal
                  /gene="CK2"
          BASE COUNT      531 a 460 c 414 g 559 t
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Query Match      16.8%; Score 181.4; DB 12; Length 1964;
Best Local Similarity 57.5%; Pred. No. 7.3e-35;
Matches 326; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

```



```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

nucleic - nucleic search, using sw model
n on: November 15, 2000, 11:23:05 : Search time 749.05 Seconds
      (without alignments)
      8914.533 Million cell updates/sec

tlo: us-09-359-026-1
rfect score: 1080
quence: 1 gtcgacccacgcgtccgaga.....tggagatacatcaaacatt 1080

oring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

arched: 7189864 seqs, 3091403243 residues

tal number o: Hits satisfying chosen parameters: 14379728

imum DH seq length: 6
imum DH seq length: 2000000000

st-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

tabase :
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
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91: gb_gss4:*
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93: em_gss2:*
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96: gb_gss5:*
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111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*
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421 GCCTCGATCTCATTTTAAATTTGATCTTCCACAGTCGATGCTTATGATGGACAG 480
589 catgaatggtgcaatca 606
111 |||||
481 CATTAATGGTGCAACA 498

SULT 2
551311 431 bp mRNA EST 23-JUL-2000
LOCUS AV551311 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION cDNA clone R2125a09R 5', mRNA sequence.
VERSION AV551311
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 431)
REFERENCE Asanizu,E., Makamura,Y., Sato,S. and Tabata,S.
AUTHORS A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
TITLE DNA Res. 7, 275-280 (2000)
JOURNAL Contact: Erika Asanizu
COMMENT The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asanizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..431
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3762"
/clone_lib="R2125a09R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/vector="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 110 a 63 c 114 g 144 t
ORIGIN
Query Match 39.9%; Score 431; DB 19; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
347 tggatcgaactgatacgaaggctcgaagctgaagtgagatggagggatgatacgt 406
|||||
1 TGGAAATCGGAACATGATAGTAAAGGCTCATGTGAGTGGATCGGACCGGAGCGTGATGATCGT 40
|||||
407 cgtgagatctctgggttttgaatttgaagggaatgattctctctgaagctgagatgaac 466
|||||
61 CGTGGATCTCTTGTTTGTAAATTTGAGAGGGAATGATTTCTTCGTGAAGTGAAG 120
|||||
467 attatctcaagatgattccatctcttggttggttaagtgagtcgaagtcacctactgatt 526
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121 ATTATATTCAGATGATATTCATCTTTGTGTTGTAGTGGTCAAGTCCCTTACTATGATT 180
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527 atgcacttgatcctcatttgaatgttgatgctcccaacagtgagatgatttactgataac 586
|||||
181 ATGCATCTGATCTCAITTTAGATGTTGATGCTTCCACACAGCTGAGATCTTTACTGATGAAC 240
|||||
587 agcatgaatggtgaatcagatcagatgagatgclataatgcttattatcagtcgltaca 646
|||||
241 AGCATGAATGGTGGAAATCAGTCGTCGAGATGATATGTTGTTTATTCATGTTGCTGATCA 300
|||||
647 ttttgactactaaaggaatggatgcaatgactgagagatcaagaactgatttctggga 706
|||||
301 TTTTGACTACTAAAGGAATGGTGCATGATGACTGAGAAGTACAAGAAGACATGATTTCGGGA 360
|||||

```


Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;
Fabales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 903)

Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V.,

Erpelting, J., Rapp, C., Shoop, E., Pardini, J., Liu, L., and Lewin, B.

A Functional Genomics Program for Soybean (NSF 9872565)

Unpublished (1999)

Title: Vodkin, L.O., P., A Functional Genomics Program for

Soybean (NSF 9872565)

Lewin, B. A., Director, Keck Center for Comparative and Functional

Genomics

University of Illinois

Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA

Tel: (217) 244-6147

Fax: (217) 333-4562

Email: l-vodkin@uiuc.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134. For further information

call: (800) 430-0030 or (314) 427-3222 FAX: (638) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or info@genome

systems.com web site: www.genomesystems.com

Seq primer: 5'-TTTTTTTCTTTTCTTTT(A/C/G)-3'

Location/Qualifiers

..803

/organism="Glycine max"

/cultivar="Williams"

/db_xref="taxon:3847"

/clone_lib="cd-1821"

/tissue_type="root"

/lab_host="XL20-Gold"

/note="Vector: p Bluescript II XR; Site: 1: EcoRI; Site: 2:

XhoI; Library Gm-r1021 is a sequence-driven, rereacted set

of the original library Gm-cl004 which was prepared from

root cDNA. The mRNA was isolated from entire roots of 8

day old 'Williams' seedlings which were propagated on

paper towels with distilled water. Stratagene's cDNA

Synthesis kit (catalog #200431) was used to synthesize

the cDNA. The Gm-cl004 library was constructed by Dr.

Paul Keim & Virginia H. Corryell, Department of Biology,

Box 5640, Northern Arizona University, Flagstaff, AZ 86011

; email: paul.keim@na.u.edu, virginia.corryell@na.u.edu. The

contig analysis to select unique genes was performed by

the laboratory of Ernest Retzel, Computational Biology

Centers, University of Minnesota,

http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html

Retracking was performed by Genome Systems, St. Louis,

http://www.genomesystems.com, and sequencing by the Keck

Center for Comparative and Functional Genomics,

University of Illinois,

http://www.life.uiuc.edu/biotech/keck.html."

241 a 173 c 150 g 222 t 27 others

Query Match 30.7%; Score 331.8; DB 21; Length 803;

Best Local Similarity 73.8%; Pred. No. 2.9e-82;

Matches 405; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

428 atttgaaggggaatattcttcttgtaagcgaatgaatataattcaaatatttca 467

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

600 ATCTCAGAGGGAATGAGTCTNNITGTGAGGTGGATGATATNNATACAGATGNNTTIN 741

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

488 acitcttgatgaagtggaagccttactatgattatgaatctgaatctttag 547

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

740 NNNATGTGGGTGANNAGTCAGTSCCTCTACTATGANNATGCCCTTCAATNNANNNG 681

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

548 atgttgatgcttccacagatgagatttactgalyaacagcatgaatgagatcaag 607

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

680 AGCTGAGTGTGCTGATGTCAGATGTCACGAGGAGACAGATGATGATGATGATGATG 621

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

608 ctgctlgagatgctataggtctcttactgcttctgcttcttacttacttacttactt 557

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

620 CGCGGGAATGCTTTATGCTGATTCATGCGAGATATGCTGTGACCAAGGAATGG 551

QY 668 ctgcaatgactagaagtaagaagtaagctgatttctggggagatgcccgagagatttctgtt 727

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 560 CTGCCATGCTTGCACAAATCAAGAACTATGATTTTGGCAGATGCCCAAGATTACTGCT 501

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 728 gcggtcagctctcttctcagcttgagacaatccgatacccgagatcgatctggaaga 787

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DB 500 CTGGACAGCGCTTCCAGTTGGTCAATCAGACATTCCTAGGTCACATCTGTCGAAA 441

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 786 tatactgcccataatcgagagatatacttaccgcgactataatcccaaggaactattg 847

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DB 440 TATATGCGCTAGCTGTGAAGATCTTACTATCCAGTTCAGATATCAAGCAACATG 381

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 848 atggagcgtactttggaacacacalccctcaactgttcttgatgacttacyggaacttaa 907

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 380 ATGGGGCTTACTTTGGAACATACATTTCCACACTCTCTTTGATGACTTAIGGCAACTGA 321

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 908 agcgcgagagccttactcaagctatgtcccaaaaatttttgcttcaagggtacacaaac 967

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DB 320 AGCCACAGAAACCCAGCACAGGCTAICTCCAGAGATTCTGGGTCAAGTTCACAACG 261

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QY 968 catgatact 976

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DB 260 CATAAAGCT 252

RESULTS 8

745989

EXONS

DEFINITION

745989 377 bp mRNA EST 04-AUG-1998

9252 Lambda-PRL2 Arabidopsis thaliana cDNA clone 136M317, mRNA

sequence.

ACCESSION

745989

VERSION

745989.1 GI:2762692

KEYWORDS

EST.

SOURCE

thale cress.

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 377)

AUTHORS

Newman, T., deBrujn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh

J., Ohlroge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel

K. and Somerville, C.

TITLE

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

JOURNAL

95148729

MEDLINE

COMMENT

On Jan 9, 1998 this sequence version replaced gi:934237.

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.

Lansing, MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn@bm.ci.msu.edu

Seq primer: T7 dye primer.

Location/Qualifiers

1..377

FEATURES

Source

/organism="Arabidopsis thaliana"

/strain="var columbia"

/db_xref="taxon:3702"

/clone="136M317"

/clone_lib="Lambda-PRL2"

/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;

lambda PRL2 is a cDNA library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

day germinated etiolated seedlings; 2) tissue culture

grown roots; 3) staged plants half with 24 hour light

cycle, half on 16 hr light, 8 hour dark- rosettes; 4)

same plants as 3 but aerial tissue (stems, flowers and

siliques. The vector is BRU's lambda zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms using

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/clone="132022T7"
/clone_lib="Lambda-PRL2"
/clone_vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRU's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA.
BASE COUNT      95 a      59 c      85 g      133 t      14 others
ORIGIN

Query Match      29.8%; Score 321.4; DB 39; Length 386;
Best Local Similarity 94.4%; Pred. No. 1.9e-79;
Matches 337; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

QY 306 ccttttcttcacatctactaaactcgaagcttcctcgatgaggaatcggaactgagtag 367
DB 1 ccttttcttcacatctactaaactcgaagcttcctcgatgaggaatcggaactgagtag 60
QY 368 aagggctcgaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 427
DB 61 aagggctcgaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 120
QY 428 atttgaaggggaatgatllcttctctgagtgagtgagtgagtgagtgagtgagtgag 487
DB 121 atttgaaggggaatgatllcttctctgagtgagtgagtgagtgagtgagtgagtgag 180
QY 488 atcttttggttttaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 547
DB 181 atcttttggttttaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
QY 548 atgttgaatgcttcccaacagtgagtgagtgagtgagtgagtgagtgagtgagtgag 607
DB 241 atgttgaatgcttcccaacagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
QY 608 ctgctgagatgctatgatgctc--ttattcattgcttgcattttgactactaaagg 662
DB 301 ctgctgagatgctatgatgctc--ttattcattgcttgcattttgactactaaagg 357

RESULT 10
AW277268
LOCUS
DEFINITION
Gm-c:019-2405 5' similar to SW:KC2C_ARATH P40229 CASEIN KINASE II
BETA' CHAIN ; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE
1 (bases 1 to 498)
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corveill,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,I., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Willson,R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

TITLE
JOURNAL
COMMENT

```

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

Insert Length: 895 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 442.

Location/Qualifiers

FEATURES

source

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/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-2405"

/clone_lib="Gm-cl019"

/tissue_type="Immature seed coats of greenhouse grown

plants"

/lab_host="DH10B (Gibco BRL)"

/note="Vector: pSPORT1 (Life Technologies); Site_1: Not I;

Site_2: Sal I; This cDNA library was constructed from mRNA

isolated from Immature seed coats (200-500 mgs) of

greenhouse grown plants. The library was prepared using

the Life Technologies pSuperScript cDNA library

construction kit. Complementary RNA was synthesized from

mRNA using a poly (dT) sequence with a Not I restriction

site. Sal I linker adapters were ligated to the

blunt-ended cDNA fragments followed by Not I digestion.

The cDNA fragments were directionally cloned into the Not

I-Sal I restriction site of the pSPORT1 vector. The

ligated cDNA fragments were transformed into E.coli

ElectroMax DH10B host cells (Gibco BRL). This library was

constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

138 a 107 c 115 g 138 t

SE COUNT

[Gin

Query Match

est Local Similarity 28.1%; Score 303; DB 21; Length 498;

Matches 372; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

490 cttgtgtgttaagtcgaagtccttactatgattgattgacactgtatctctttagat 549

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1 CTATGTGGTGTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 60

550 attgactcttccacactgagatgatttactgattgacacagatgaaaggtggaatcagct 609

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

61 GTGAGCTCGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

610 gctgagatgctatagctcttattatcattgcttacttacttacttacttacttactt 659

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

121 CCGGAATGCTTTATGCTCTGTTTCATGCGCAGATATGTTGACCAACAGAGNATGGCT 180

670 gcaatgactgagaagtcacagaactgctgatttggggagatgcccagagagtttctgttgc 729

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

181 GCGATGCTTGACAAATACAGAACTATGATTGACAGATGCGCCAGAGTTCATCTCT 240

730 gattcaactcttcttcaacttgcacacacacacacacacacacacacacacacacac 789

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

241 GACAGACCTCCCTTCCAGTTGGTCAATACAGACATGCTTACGATCAATGTCGCAAAATA 300

790 tactgcccctaaatgacagatatacttaccgacatctaaatctcgaagcaatattgat 849

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

301 TATGTCCTTAGTGTGAGATCTTTTACATATCCAGCTTCCCAAGTATCAGGCAACATGAT 360

850 ggaagcttacttggaaacacatcccttcccttcttcttcttcttcttcttcttcttctt 909

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

361 GGGGCTTACTTTGGAACTACATTTCCCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

910 ccgcagaaagcactaaagcattatgccccaaaaatcttcttcttcttcttcttcttcttctt 959

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

421 CCACAGAAACAGCAGCAAGGCTATGTTCCCAAGAGTCTTTGGGTTTCAAAGTTCACAGCCCA 480

Qy 970 t-gatact 976

||| |||

Db 481 TAAAGCT 487

RESULT 1:

AW433059

LOCUS

DEFINITION

HTA CHAIN 1, mRNA sequence.

ACCESSION

AW433059.1 GI:6964366

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Glycine max

soybean.

REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna

A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,

Wyllie,T., Underwood,K., Steptoe,M., Jheising,B., Allen,M., Bowers

Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk

R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann

R., Waterson,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

Insert Length: 603 Std Error: 0.00

High quality sequence stop: 449.

Location/Qualifiers

1..655

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl029-203"

/clone_lib="Gm-cl029"

/tissue_type="very young cotyledons of greenhouse grown

plants"

/lab_host="DH10B"

/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; This

cDNA library was constructed from mRNA isolated from very

young cotyledons (20-50mgs fresh weight) of greenhouse

grown plants. The library was prepared using the Life

Technologies pSuperScript cDNA library construction kit.

Complementary DNA was synthesized from mRNA using a

poly(dT) sequence with a Not I restriction site. Sal I

linker adapters were ligated to the blunt-ended cDNA

fragments followed by Not I digestion. The cDNA fragments

were directionally cloned into the Not I-Sal I restriction

site of the pSPORT1 vector. The ligated cDNA fragments

were transformed into E.coli ElectroMax DH10B host cells.

This library was constructed by Dr. Paul Keim and Dr.

Virginia Coryell."

BASE COUNT

ORIGIN

196 a 131 c 154 g 172 t 2 others

Query Match

Best Local Similarity 26.9%; Score 290.6; DB 22; Length 655;

Matches 362; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

```

332 ctcagcttctctgatgagggaatcggaaactatagtaaaagggtcctgatgtgagatgagatg 391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 CTAACTCAATACAGGAGGATTTGAAACAAAGATGTCGAAGTACTGATGTTAGTCTTTTCA 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
392 aggggtgatgatacgtcgtggtgattctcttggctttgttaatttgagaggaagattctctt 451
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
222 AAGGGGAIGACACAICTTGGATCTCATGGTTTTCGAATTTGACAGCAAAATGAATTCWTTT 281
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
452 ggaagucagaaagatallatcaagatgatttcaatttttqgqllaaqgagcaag 511
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
282 GCGAAGTTCATGATGATTTGCGGCAAGATGATTTCAAGCTCTCTGGATTAAGTAGTCAAG 341
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
512 tcccttactatgallatgcaactgattctctatctttagatgtttagctttcccaacagtgaga 571
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
342 TCCCTACTATCATGATATGACATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 401
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 tatttactatgaagacatgaatgggtggaatcagctgctgagatgctatggtcttta 631
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
402 CTTTCAGGAGGACCAAAATGAGTTAAATTTGAATCTGCAGACAAATGCTNTATGGTCTCA 461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 tttactatgaagacatgaatgggtggaatcagctgctgagatgctatggtcttta 631
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462 TTCAATGCCCGATACATTTTCACAAAGCAAAAGGAATGGCTGCAATGCTTCACAAAGTCA 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
692 actgtgatttcgggagatcccgagaggtttctgttggctgagctgctgctgctgctgctg 751
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
522 ACTACAAATTTGGCGGATGCTCAAGATNTTCTGCTCTCGACAAACCCCTCCCTCGCGGTG 581
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
752 gacaatccgatcccgagatgagtaactgtgaaagataactgacctaaatcgaggata 811
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
582 GCCAGTCACAIGTCTTAGTCAAGTACTCTAAAGATATATTGCCCCAGGTCTGAGGACA 641
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
812 tat 814
   |||
642 TGF 644
   |||

```

ULF 12

71192

US

INITIATION

SSION

SION

WORDS

RCE

RGANISM

ERENCE

AUTHORS

TITLE

CURL

MENT

Seq primer: T3

High quality sequence stop: 511.

Location/Qualifiers

1. 543

/organism="Beta vulgaris"

/cultivar="USH20"

/db_xref="taxon:3555"

/clone="103"

/clone_lib="Sugar Beet germination cDNA library"

SOURCE

RESULTS

BE405491

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

/tissue_type="whole seedlings"

/dev_stage="4-day germination under stress (salt/NaCl,

dehydration/Mannitol and anaerobic stress)"

/lab_host="SOLR"

/note="Organ: seeds; Vector: pBluescript II KS (+) excised
from Lambda Uni-zap XR; Site_1: EcoRI; Site_2: XhoI; cDNAs
were derived from reverse transcription of pooled mRNA
samples from stressed seedlings (germinated for 4 days in
150mM NaCl, 200mM Mannitol, submerged in distilled water
and 0.3% hydrogen peroxide). The cDNA library was
generated by directional ligation of the cDNAs in the
EcoRI and XhoI sites of Lambda Uni-zap XR vector
(Stratagene). The library was excised as a pBluescript
plasmid from Lambda Uni-zap XR by EXAssist helper phage
and plated on SOLR host cells."

BASE COUNT 160 a 104 c 121 g 158 t

ORIGIN

```

Query Match      26.6%; Score 286.8; DB 24; Length 543;
Best Local Similarity 72.6%; Pred. No. 1.1e-69;
Matches 405; Conservative 0; Mismatches 137; Indels 16; Gaps 2;

QY 387 atcgagggtgatgatacgtcgtggtggtctctctgtttgttaattgagaggaatgattt 446
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 ATCTGATGGTGAGGATACAGCATGCGATTTCATGGTTTGCATTTGCCAGGCAATGAAT 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 447 cttctgtgaagtcgagaaallalaticcaagatgatttcaacttltglttaagtg 506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TTTCTGTGAGATTGATGATTTACATCCAAAGATTTCAATCTTTGTGATTTGAGCAG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 507 tcaagctccttactatgattgactgactgactcctttagatgtttagatgttgcctccacag 566
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CCAAGTTCCATTTATGATTACGCACTCGACGTCATTTTGAATTTGAATCTTC----- 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 tgagatgtttactatgatacagcagcatggaatggtggaatcagctgctgagatgctatatgg 626
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 -----TCATGAGGAACAGATGAGTTGATTCAATCTGCGGCAGAAATGCTTTATGG 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 627 tcttattcatgttcttaccattttgaactactaaagagagcgcgcaatgacgagaagata 686
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 CCGTGTATGATGTCGATCATATTTGACTAGTAAAGGAATTTGCTATGTAAAGAAAGAA 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 687 caagaactgtgatttcggagatgcccagagagtttctgttgcggtcagctcttctctcc 746
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 TAAAAAANATGAAATTTCCGGCTTGTCACAGGATTTACTGCTCTGCGCAGGC-GGCTTTCC 344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 747 agttggacaatccgatacccggagatgagtagtactgtgagatatactgctttaaagcga 806
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 345 GTTGGCCCATCAGACATTCACGATCAAGCACCCGTGAAATCTACTGCCCAAAATGTCA 404
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 807 quatatacttaccgcgacalctaaattccaaagcaaatattgatgagcglatcttggaac 866
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 405 AGACATCTATCAACCAAGTCGAAATACCAAGCAATGTGGTGGTATCATATAGGAC 464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 867 cacatccctcactgttctctgactgactacgaggaactaaagccgagaagcctactca 926
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 465 TCAATTCCTCACTTTTCTTCGTGATACGCGCAACCTTTTGCCCACTCAAGCAACTAA 524
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 927 agctatgtcccaaaaaa 944
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 AACCTATGTCCCGAGGAT 542
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 13

BE405491

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BE405491

562 bp mRNA

EST

21-JUL-2000

WHE1216_H11_P222S Wheat etiolated seedling root cDNA library

Iriticum aestivum cDNA clone WHE1216_H11_P22, mRNA sequence.

BE405491

GI:9364959

EST.

bread wheat.

New CKB3 gene and protein sequences used to alter circadian rhythms and

atches	325: Conservative	0: Mismatches	24: Indels	0: Gaps	0:
397	gatgatacgtcgtggaatctctgggttttgaatttggagaggaatgatctctctgtgaa	456			
2912	gaggaggtctcgtggaatctctgggttttgaatttggagaggaatgatctctctgtgaa	2971			
457	gtcgtatgagattatattcaagatgatttcaattcttctgtgttgaagtggtcaagtcctt	516			
2972	gtcgtatgagattatattcaagatgatttcaattcttctgtgttgaagtggtcaagtcctt	3031			
517	tactatgattatgctcgtggtatcctatcttgaatttgaatttgaatttgaatttgaattt	576			
3032	tactatgattatgctcgtggtatcctatcttgaatttgaatttgaatttgaatttgaattt	3091			
577	actgatgacacatgaaatgatgaggaatcagctgctggaatgctggaatgctggaatgct	636			
3092	actgatgacacatgaaatgatgaggaatcagctgctggaatgctggaatgctggaatgct	3151			
637	gtctcttactatcttactatcactaagaatgaggtgctgcaatgactgagaggaagaaactgt	696			
3152	gtctcttactatcttactatcactaagaatgaggtgctgcaatgactgagaggaagaaactgt	3211			
697	gattctcggagatgcggagaaatttctatctgctggaatgctggaatgctggaatgct	756			
3212	gattctcggagatgcggagaaatttctatctgctggaatgctggaatgctggaatgct	3271			
757	tccgaatcaccgagatcagatgctggaatgctggaatgctggaatgctggaatgct	816			
3272	tccgaatcaccgagatcagatgctggaatgctggaatgctggaatgctggaatgct	3331			
817	taccctcgatcctaaatcccaaggaatgctggaatgctggaatgctggaatgct	876			
3332	taccctcgatcctaaatcccaaggaatgctggaatgctggaatgctggaatgct	3391			
877	caatctgttactatgactacaggggaacttcaaaacgcaaaagcctactcaaaagctatgic	936			
3392	caatctgttactatgactacaggggaacttcaaaacgcaaaagcctactcaaaagctatgic	3451			
937	ccaaaaatttttggcttcaaggtaca	967			
3452	ccaaagctcaggtttcaaggtaca	3477			
ULT 4					
911/c					
250911 standard; DNA: 8430 BP.					
250911:					
31-MAY-2000 (first entry)					
Recombinant human beta-casein expressing construct pRSB-14.					
Plasmid pRSB-14; recombinant; beta-casein; human;					
casein kinase II alpha subunit; casein kinase II beta subunit;					
kanamycin resistance marker; iminopeptidase; genetic stability;					
pharmaceutical; nutritional composition; vaccine formulation; ds.					
Chimeric - Lactobacillus delbrueckii.					
Chimeric - Homo sapiens.					
Chimeric - Bacteriophage T7.					
Key	Location/Qualifiers				
promoter	complement (3..103)				
	*tag= a				
	/label= Ptac_promoter				
CDS	complement (111..995)				
	*tag= b				
	/product= "L. delbrueckii Iminopeptidase"				
promoter	complement (1001..1486)				
	*tag= c				
	/label= rrrhT72_promoter				
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FT	/label= ori				
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FT	/label= T7_promoter				
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FT	complement (6084..6732)				
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FT	/product= "Casein kinase II alpha subunit"				
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FT	*tag= k				
FT	/label= T7_terminator				
XX					
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PN					
XX					
PD	17-FEB-2000.				
XX					

517 tactatgattatgacattatcattttagatgttgatgcctcraacagttatgttt 576
|||||
2214 CACTACCGACAAGCTCTAGACATGATCTTTGGACCTGGAGCCCTGATGAAATGGAAGAC 2155
577 actgatgaacagcatgaatggtgggaatcagctgctgagatgctatattgtttatcat 636
|||||
2154 AACCCCAACACAGAGTACCTGATGAGACACCGACCGACAGATCTTTATGATGATGACAC 2095
637 qttoqlaacatttactactaagaagatgagatgcaatcactgaagaagatcaagaacttgt 696
|||||
2094 GCGCGCTACATCCTTACCAACCGTGGCATCGCCCAAGATGTGGAAAGATACCCAGCAAGCA 2035
697 gatttcggagagatcccgagatgtttctgttgcggtcactgttgcctccagttcagacaa 756
|||||
2034 GACTTGGGTACTGTCTCTGCTGCTACTGTGAGACACACCCCAATCTTCCCATTTGCCCTT 1975
757 ttcgatatcccgagatcgagtagctgtagaagatatactgcccctaaatgagagatatactt 816
|||||
1974 TCAGACATCCCAAGTCAAGCCATGGTGAAGCTCTACTGCCCAAGTGCATGCTGTGATC 1915
817 taccocccqalcataattccaaaggaatattgtagagagatcttggaaaccacttccct 876
|||||
1914 ACACCCAAAGTCAATCAAGACACCATCACACGGATGGCGCTACTTCCGCACITGCTTCCCT 1855
877 cactgttcttgatgacttaacgggaacttaaaagccgcagaaagcctactcaaaagctatgtc 936
|||||
1854 CAGATGCTCTGTATGTGTGATCTCCGAGTACCGGCGCCCAAGAGACTGCCCAACCAAGTITG 1795
937 ccaaaaattcttggctcaggtaca 962
|||||
1794 CCGAGGCTCTACGGTCTCAAGATGCCA 1769

USLJ 5
406

X83406 standard; cDNA; 335 BP.

X83406;

31-AUG-1999 (first entry)

Breast cancer tumour specific clone #160.

Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
human endogenous retrovirus; vaccine; ss.

Homo sapiens.

W09725426-A2.

17-JUL-1997.

10-JAN-1997; 97WO-US00485.

20-AUG-1996; 96US-0700014.

11-JAN-1996; 96JS-0585392.

(CORI-) CORIXA CORP.

Frudakis TN, Reed SG, Smith JM;

WPI: 1997-372865/34.

Breast cancer-related DNA from retrovirus antigen (s) - useful for
diagnosis and treatment of breast cancer

Claim 21; Page 180; 22pp; English.

Sequences X83201-X83285 and X83331-X83415 represent novel breast cancer
tumour specific clones which are expressed from a genomic region
containing a human endogenous retrovirus (X83330). Detection of
the clone sequences allows determination of the presence of breast

CC cancer in a mammal. Progression of breast cancer can be monitored by
CC detecting the level of clone expression. Polypeptides encoded by the
CC clones can be used in vaccines to inhibit or prevent breast cancer.

XX Sequence 335 BP; 87 A; 84 C; 86 G; 78 T; 0 other;

Query Match 9.7%; Score 104.6; DB 18; Length 335;
Best Local Similarity 57.5%; Pred. No. 2.3e-22;
Matches 188; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 358 actgatagtgagggtctgagtgagtgaggatcgagggtgtaatacactcgtgatctct 417
Db 3 acacctgtccagcatctgacgtgaagatgagcagctcagagaggtgctcgtgattcc 62
Qy 418 tgggtttagtaattgagagggaatgatttcttctgaaagtcagatgaagattatattcaa 477
Db 63 tgggtctgtgggctccgtggcaatgaattctctgtgaagtgagtgactacatccag 122
Qy 478 gatgatttcaatcttgggttttaagtgggtcaagtcctactatgattatgcacttgat 537
Db 123 gacaaatttaacttactggactcaatgagcagtcctcactatcgacaagctctagac 182
Qy 538 ctcatttttagatgttgatgcttccacacagtgagatgtttactgatgaacagcatgaaatg 597
Db 183 atgattcgtgacctggagcctgatgaagaactggaaagacaccccaaccagatgacctg 242
Qy 598 gtgaatacagctgctgagatgctatattgttcttattcatgttcttactatgttact 657
Db 243 attgagcaggcagcagatgcttttattgattgattccacgcccgtctacatccttaccac 302
Qy 658 aaaggaatggctgcaatgactgagaag 684
Db 303 cgtggcatcgccagatgctggacaag 329

RFSULJ 6

V69018

ID V69018 standard; DNA; 335 BP.

AC V69018;

22-JAN-1999 (first entry)

DNA molecule encoding a polypeptide for detecting breast cancer #20.

Human; Breast cancer; breast tumour tissue; diagnosis; treatment;
vaccine; epitope; endogenous; retroviral element; ss.

Homo sapiens.

W09645328-A2.

15-OCT-1998.

09-APR-1998; 98WO-US06939.

11-DEC-1997; 97US-0991789.

09-APR-1997; 97US-0838762.

(CORI-) CORIXA CORP.

Frudakis TN, Reed SG, Smith JM;

WPI: 1998-557473/47.

New DNA sequences isolated from endogenous human retroviral element
- and related vectors, transformed cells, proteins and antibodies,
useful for diagnosis, treatment and prevention of breast cancer

Claim 11; Page 108; 173pp; English.

V68999 to V69038 represent nucleotide sequences which encode polypeptides

used in detecting human breast cancer. Detection or measurement of human breast tumour specific polypeptides and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and monitoring of breast cancer. Human breast tumour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs are also useful in vaccines for inhibiting development (for prevention or therapy) of breast cancer. The polypeptides may also be used to raise monoclonal antibodies, used in immunoassay reagents.

Sequence 335 BP; 87 A; 84 C; 86 G; 78 T; 0 other;

```

every Match      9.7%:  Score 104.6;  DB 19;  Length 335;
best Local Similarity 57.5%:  Pred. No. 2.3e-22;
Matches 188;  Conservative 0;  Mismatches 139;  indels 0;  Gaps 0;

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3 acacttgcaccacatctgagctgaagatgaagucctcacagaagcgtgttcaggattcc 62

418 109tttttgcgaatttcagaaagggaattgaattctctctatgaagtcgaatgaaagatataatctcaa 477

63 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

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1. **Introduction**
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 217. **Figure 209**

[illegible][illegible]

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303 cgtggcatcqcccagatgctggacaag 329

532/c

QZ5555Z STANBUD13; DNRX, 1043 DEZ.

17555570

22-NOV-1992 (first entry)

Sequence of genomic clone contg. the entire Histidine-rich

CONSTITUTION

key	location/quantity
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191567
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/*taq= b

intron 360..490

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                    /#tag= c

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mat peptide
/label ~ splice sequence
563 1477
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/*tag= i
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PN	US5116955-A.
PP	25-MAY-1992.
XX	
PP	26-AUG-1986; 86US-0900401.
XX	
PP	26-AUG-1986; 86US-0900401.
XX	
PA	(SLOK) SLOAN KETTERING INST CANCER.
XX	
PI	Pologe L, Ravetch JV;
XX	
DR	WPI: 1992-199590/24.
DR	P-PADB: R24393.
XX	
PI	Histidine-rich protein associated with plasmodium knob phenotype -
PP	and DNA encoding it, used for in vitro diagnosis of P.
P-	Falciparum infection.
XX	
PS	Disclosure: Fig 7A-B; 29pp; English.
XX	
CC	"Two variants of HisRP are produced by P. falciparum. One is
CC	associated with what is referred to as "knobby phenotype" (K30) and
CC	"knobless phenotype" (K-). The "knobby" and "knobless" phenotypes
CC	have been implicated in cytoadherence, which is characteristic of
CC	erythrocyte infection. It has now been found that cDNA expressing
CC	both K- and K- HisRP can be obtained by the use of P. lophurae HisRP
CC	expressing DNA. The genomic clone (Q25532) is encoded in two
CC	exons, separating the signal peptide-encoding sequence from the
CC	pro-sequence, confirming that synthesis of the protein occurs via
CC	the preproprotein. Oligo. probes synthesised to the signal
CC	peptide-encoding exon reveal multiple homologous DNA sequences in:
CC	the P. lophurae genome. The sequence of mature proteins is arranged
CC	in numerous tandem repeats with; up to nine histidine residues in a
CC	row, similar to other Plasmodium proteins for which sequence data
CC	have so far been reported.
XX	
SO	Sequence 1648 BP: 569 A: 486 C: 150 G: 441 T: 0 other:

Query Match 3.4%; Score 36.4; DB 13; Length 1648;
Best Local Similarity 45.9%; Pred. No. 0.37;
Matches 124; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

[illegible]

RESULT	8
Q80911/C	
ID	Q80911 standard; CDNA; 5181 BP.
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AC	Q80911;
XX	
XX	
DC	24-AUG-1995 (first entry)
XX	
XX	

04-MAY-1999 (first entry)

Mouse pheromone receptor VR2 coding sequence.

Pheromone receptor; signal transduction; fertility; behaviour;
reproduction; rodent; insect; mouse; ss.

Mus sp.

W09900422-A1.

07-JAN-1999.

30-JUN-1998; 98WO-US13680.

30-JUN-1997; 97US-0051284.

(HARD) HARVARD COLLEGE.

Buck L, Dulac C, Herrada G, Matsunami H;

WPI: 1999-095684/08.

P-PSDB; W94912.

New isolated pheromone receptor polypeptides - used to develop
products for controlling fertility and behaviour in vertebrates and
invertebrates

Claim 23; Page 178; 308pp; English.

The invention relates to polynucleotide sequences encoding mammalian
pheromone receptor polypeptides. The polypeptides are expressed in
murine and rat vomeronasal organ. The products can be used for modifying
pheromone activity, e.g. for decreasing pheromone receptor mediated
signal transduction. They can be used for controlling fertility and
behaviour in vertebrates and invertebrates. Compositions comprising the
polypeptides are particularly useful in e.g. controlling fertility in
livestock and controlling reproduction in rodents or insects by
interrupting the normal behaviours of rodents or insects that result in
reproduction. The present sequence represents the coding sequence of
mouse pheromone receptor VR2.

Sequence 2424 BP; 682 A; 487 C; 504 G; 751 T; 0 other;

Query Match 3.2%; Score 34.8; DB 20; Length 2424;
Best Local Similarity 52.0%; Pred. No. 1.4;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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130 agggagtgtctatttacccttggaaaactaatgaaccattggaagatagtttataat 189
493 tctgatttaagtggtcaagtccttactatataattatgaacttgatctcaatttagatgttt 552
150 tatgatttaagttttagaattgcagggaagtgaatagcttctctgtgtaattgttttt 249

553 gatgcttccaacagtcgagatattactgat 582

250 gctactgagatgagatcaacaagaatccttat 279

15

372

X05812 standard; cDNA; 2821 BP.

X05812:

04-MAY-1999 (first entry)

Mouse pheromone receptor VR12 encoding cDNA.

Pheromone receptor; signal transduction; fertility; behaviour;
reproduction; rodent; insect; mouse; ss.

Mus sp.

Key Location/Qualifiers
CDS 60..995
/*tag= a

W09900422-A1.

07-JAN-1999.

30-JUN-1998; 98WO-US13680.

30-JUN-1997; 97US-0051284.

(HARD) HARVARD COLLEGE.

Buck L, Dulac C, Herrada G, Matsunami H;

WPI: 1999-095684/08.

P-PSDB; W94912.

New isolated pheromone receptor polypeptides - used to develop
products for controlling fertility and behaviour in vertebrates and
invertebrates

Claim 15; Page 106-108; 308pp; English.

The invention relates to polynucleotide sequences encoding mammalian
pheromone receptor polypeptides. The polypeptides are expressed in
murine and rat vomeronasal organ. The products can be used for modifying
pheromone activity, e.g. for decreasing pheromone receptor mediated
signal transduction. They can be used for controlling fertility and
behaviour in vertebrates and invertebrates. Compositions comprising the
polypeptides are particularly useful in e.g. controlling fertility in
livestock and controlling reproduction in rodents or insects by
interrupting the normal behaviours of rodents or insects that result in
reproduction. The present sequence represents a cDNA encoding a mouse
pheromone receptor VR12. The cDNA is deposited under the Genbank
accession number AF011422.

Sequence 2621 BP; 809 A; 568 C; 561 G; 883 T; 0 other;

Query Match 3.2%; Score 34.8; DB 20; Length 2821;
Best Local Similarity 52.0%; Pred. No. 1.5;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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493 tctgatttaagtggtcaagtccttactatgattgacttgatctcaatttagatgttt 552
249 tatgatttaagttttagaattgcagggaagtgaatagcttctctgtgtaattgttttt 308

553 gatgcttccaacagtcgagatgtttactgat 582

309 gctactgagatgagatcaacaagaatccttat 338

Search completed: November 15, 2000, 12:58:26

Job time: 5482 sec

